

SEARCH REQUEST FORM

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Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 02-24-03

Searcher: Beserly 4994

Terminal time: 20

Elapsed time: _____

CPU time: _____

Total time: 23

Number of Searches: _____

Number of Databases: 1

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG Suite

_____ STN

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_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

_____ ☒ Other CGN

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OM protein - protein search, using sw model

Run on: February 24, 2003, 09:19:21 ; Search time 39 Seconds
(without alignments)
2364.344 Million cell updates/sec

Title: US-09-608-918-2
Perfect score: 3716
Sequence: 1 MPVPWFLLSLALGRSPVLS.....TPAPRGVGPAGPCAGDGT 692

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
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9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3716	100.0	692	22	Human cytokine rec
2	3716	100.0	692	23	Human cytokine rec
3	3699.5	99.6	705	22	Human PRO polypept
4	3699.5	99.6	705	22	Human interleukin
5	3699.5	99.6	705	22	Human interleukin
6	3699.5	99.6	705	22	Human PRO20040. H
7	3699.5	99.6	705	22	Chimeric Zcytor14
8	3699.5	99.6	705	23	Human anglogenesis
9	3699.5	99.4	705	23	Human PRO20040 pro
10	3654	98.3	720	23	Human interleukin
					Human full length

11	3604.5	97.0	675	22	AAB61885
12	3588	96.6	688	22	AAB61883
13	3566.5	96.0	703	23	AAU98791
14	3535.5	95.1	703	23	AAU11353
15	3510.5	94.5	693	23	AAU98790
16	3445.5	92.7	683	23	AAU98789
17	2971	80.0	575	22	AAB61881
18	2576.5	69.3	553	23	AAU98788
19	2410.5	64.9	698	23	AAU11354
20	2408.5	64.8	698	23	ABT72237
21	2400.5	64.6	698	23	AAU99161
22	2389.5	64.3	698	23	AAE14560
23	2352.5	63.3	674	23	AAE14559
24	2006.5	54.0	409	23	AAU98787
25	1886	50.8	372	23	AAU98786
26	1714.5	46.1	348	23	AAU98785
27	1432	38.5	309	21	AAU76143
28	1365.5	36.7	332	23	AAU98784
29	1305	35.1	267	22	AAU98782
30	1300	35.0	332	22	AAU25864
31	1266	34.1	269	23	AAU98783
32	1079	29.0	204	22	AAE10920
33	933	25.1	186	23	AAU98782
34	326.5	8.8	617	21	AAU76048
35	326.5	8.8	617	22	AAU55987
36	326.5	8.8	617	22	ABT72187
37	309.5	8.3	667	22	AAU04957
38	309.5	8.3	667	23	AAU83601
39	304.5	8.2	657	23	AAU11356
40	174	4.7	866	17	AAU04185
41	174	4.7	866	19	AAU61272
42	174	4.7	866	20	AAU92409
43	174	4.7	866	21	AAU99941
44	174	4.7	866	21	AAU97131
45	174	4.7	866	21	AAU97181

ALIGNMENTS

RESULT 1
AAB61880
ID AAB61880 standard; Protein; 692 AA.
XX
AC AAB61880;
XX
DT 08-MAY-2001 (first entry)
XX
Human cytokine receptor Zcytor14.
XX
Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
KW antiinflammatory; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PW WO200104304-A1.
XX
PD 18-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US18383.
XX
PR 07-JUL-1999; 99US-0348854.
XX
(ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Burkhead SK, Pownder SL;
XX
DR WPI; 2001-112618/12.
XX
N-PSDB; AAC85027.
XX
New polypeptide encoding a human cytokine receptor Zcytor14, for
treating inflammation e.g. rheumatoid arthritis -

Chimeric Zcytor14
Chimeric Zcytor14
Human interleukin
Human DNAX cytokin
Human interleukin
Human interleukin
Human variant Zcyt
Human interleukin
Mouse DNAX cytokin
Murine protein iso
Murine interleukin
Murine cytokine re
Murine cytokine re
Human interleukin
Human interleukin
Human secreted pro
Human interleukin
Human membrane or
Human protein sequ
Human interleukin
Human gene 12 enco
Human interleukin
Murine skin cell p
Skin cell protein,
Murine protein iso
Human interleukin
Human PRO protein,
Human DNAX cytokin
Human interleukin-
Human interleukin-
Human IL-17R prote
Human IL-17R prote
Human interleukin-
Human interleukin-

PS Claim 2; Page 2; 112pp; English.

XX The invention provides a new human cytokine receptor designated zcytor14.

CC zcytor14 can be expressed by standard recombinant methodology. The

CC encoding nucleic acid is useful for detecting the expression of a

CC zcytor14 gene in a biological sample. Anti-zcytor14 antibodies can be

CC used to screen biological samples in vitro for the presence of zcytor14.

CC Proteins, polypeptides and peptides having zcytor14 activity can be

CC administered to a subject who lacks an adequate amount of this

CC polypeptide, for treating inflammation and conditions such as rheumatoid

CC arthritis. In contrast, zcytor14 antagonists (e.g. anti-zcytor14

CC antibodies) can be used to treat a subject who produces an excess of

CC zcytor14. zcytor14 nucleotide sequences can also be used to provide

CC zcytor14 to a subject. The present sequence represents the human

CC cytokine receptor zcytor14.

XX

XX Sequence 692 AA;

Query Match 100.0%; Score 3716; DB 22; Length 692;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPVPWFLLSLALGRSPVLSRLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAGPV 60

Db 1 MPVPWFLLSLALGRSPVLSRLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAGPV 60

QY 61 LAPHLQTELVLRCQKEDCDLCLRVAVHLAVHGHWEPEDEKFGGAADSGVEPRNAS 120

Db 61 LAPHLQTELVLRCQKEDCDLCLRVAVHLAVHGHWEPEDEKFGGAADSGVEPRNAS 120

QY 121 LQAQVLSFQAYPTARCVLLEQVPAALVQFGSGVSVYDCFEAALGSEVIRWSYTOPR 180

Db 121 LQAQVLSFQAYPTARCVLLEQVPAALVQFGSGVSVYDCFEAALGSEVIRWSYTOPR 180

QY 181 YEKELNHTQOLPALPWLNVNSADGNVHLVNSVEQHFGLSLYNQVGGPPKPRHKNLT 240

Db 181 YEKELNHTQOLPALPWLNVNSADGNVHLVNSVEQHFGLSLYNQVGGPPKPRHKNLT 240

QY 241 GQIITLNTHTDVLPCICIQWPLEPDSVRTNICPFREDPRAHQLWQAARLLTLQSWL 300

Db 241 GQIITLNTHTDVLPCICIQWPLEPDSVRTNICPFREDPRAHQLWQAARLLTLQSWL 300

QY 301 LDAPCSLPAEALCWRAAGDPCQPLVPPLSWENVTVDKVFLLKGNPLCVQVNSSE 360

Db 301 LDAPCSLPAEALCWRAAGDPCQPLVPPLSWENVTVDKVFLLKGNPLCVQVNSSE 360

QY 361 KLQLOECLWADSLGPKDDVLLLETRGPQDNRSICALPESGCTSLPSKASTRAARLGEYL 420

Db 361 KLQLOECLWADSLGPKDDVLLLETRGPQDNRSICALPESGCTSLPSKASTRAARLGEYL 420

QY 421 LODLQSGQCQLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKA 480

Db 421 LODLQSGQCQLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKA 480

QY 481 AARGRAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELSAQGPVAFHQAORR 540

Db 481 AARGRAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELSAQGPVAFHQAORR 540

QY 541 QTLQEGGVVLLFSPGAVALCSWLDQVSGGAGHPDFAFRASLSCVLPDFLQGRAPGS 600

Db 541 QTLQEGGVVLLFSPGAVALCSWLDQVSGGAGHPDFAFRASLSCVLPDFLQGRAPGS 600

QY 601 YVACFDRLHDPVAPALPRTVPVFTLPOLPDFLQALQOPRAPRSRGLQERAEQVSRA 660

Db 601 YVACFDRLHDPVAPALPRTVPVFTLPOLPDFLQALQOPRAPRSRGLQERAEQVSRA 660

QY 661 QPALDSYFHPGCTPAPGRGVGAGPGAGDGT 692

Db 661 QPALDSYFHPGCTPAPGRGVGAGPGAGDGT 692

RESULT 2

AAE14562

ID AAE14562 standard; Protein; 692 AA.

XX AAE14562;

AC AAE14562;

DT 17-MAY-2002 (first entry)

XX Human cytokine receptor zcytor14.

DE Murine; cytokine receptor; zcytor14; inflammation; rheumatoid arthritis;

KW gene therapy; protein therapy; human; receptor.

XX Homo sapiens.

OS WO200204519-A2.

PN 17-JAN-2002.

PD 05-JUL-2001; 2001WO-US21344.

PF 06-JUL-2000; 2000US-216446P.

PR (ZYMO) ZYMOGENETICS INC.

XX Gao Z;

PI WPI; 2002-179701/23.

DR New murine cytokine receptor, zcytor14, and polynucleotides encoding

PT the receptor, useful for treating inflammation, specifically rheumatoid

PT arthritis, and as educational tools or in research -

XX Disclosure; Page 98-99; 99pp; English.

XX The invention relates to murine cytokine receptor, zcytor14.

CC The zcytor14 polypeptide is useful for identifying or isolating

CC zcytor14 ligands, in preparing antibodies, in identifying proteins or

CC peptide cleavage sites, in amino acid sequence analysis, and in

CC monitoring biological activities of both the native and tagged protein in

CC vitro or in vivo. Polypeptides having zcytor14 activity can be used to

CC treat inflammation, such as rheumatoid arthritis. zcytor14 polynucleotide

CC may be used as educational tool in genetics, molecular biology,

CC protein chemistry and antibody production analysis, in the preparation

CC of expression constructs for bacterial, viral or mammalian expression,

CC in determining mRNA and DNA localisation of zcytor14 polynucleotide in

CC tissues, for identifying related polynucleotides and polypeptides by

CC nucleic acid hybridisation, in linkage-based testing for various

CC diseases in murine models, and to determine whether a subject's

CC chromosomes contain a mutation in the zcytor14 gene. zcytor14

CC oligonucleotide probes are useful for in vivo diagnosis, and for

CC detecting and localising zcytor14 gene expression in tissue samples.

CC The present sequence is human cytokine receptor, zcytor14 which can

CC be used to generate humanised variant of murine zcytor14 sequence.

XX

SQ Sequence 692 AA;

Query Match 100.0%; Score 3716; DB 23; Length 692;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPVPWFLLSLALGRSPVLSRLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAGPV 60

Db 1 MPVPWFLLSLALGRSPVLSRLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAGPV 60

QY 61 LAPHLQTELVLRCQKEDCDLCLRVAVHLAVHGHWEPEDEKFGGAADSGVEPRNAS 120

Db 61 LAPHLQTELVLRCQKEDCDLCLRVAVHLAVHGHWEPEDEKFGGAADSGVEPRNAS 120

QY 121 LQAQVLSFQAYPTARCVLLEQVPAALVQFGSGVSVYDCFEAALGSEVIRWSYTOPR 180

Db 121 LQAQVLSFQAYPTARCVLLEQVPAALVQFGSGVSVYDCFEAALGSEVIRWSYTOPR 180

QY 181 YEKELNHTQOLPALPWLNVNSADGNVHLVNSVEQHFGLSLYNQVGGPPKPRHKNLT 240

Db 181 YEKELNHTQOLPALPWLNVNSADGNVHLVNSVEQHFGLSLYNQVGGPPKPRHKNLT 240

Db	181	YEKELNHTQOLPALPWLNVNSADGDNVHLVNVSEBQHFGLSLYWNVOGPPKPRWHKNLT	240
Qy	241	GPQIITLHNHTDLVPCICIQVWPLESDSVRTNCFREDPRAHONLWQAARLLTLQSWL	300
Db	241	GPQIITLHNHTDLVPCICIQVWPLESDSVRTNCFREDPRAHONLWQAARLLTLQSWL	300
Qy	301	LDAPCSLPAAALCWRAAGDPCOPLVPPLSWENVYDKVLEFPLKKGHPNLCVQVNSSE	360
Db	301	LDAPCSLPAAALCWRAAGDPCOPLVPPLSWENVYDKVLEFPLKKGHPNLCVQVNSSE	360
Qy	361	KLQLOECLWADSLGPKDDVLLLETRGPQDNRSICALPEPSGCTSLPSKASTRAARLGEYL	420
Db	361	KLQLOECLWADSLGPKDDVLLLETRGPQDNRSICALPEPSGCTSLPSKASTRAARLGEYL	420
Qy	421	LQDLSQCQLQWDDDLGALWACPMKYIHKRWALVWLACLLFAAALSILLKKDHAKA	480
Db	421	LQDLSQCQLQWDDDLGALWACPMKYIHKRWALVWLACLLFAAALSILLKKDHAKA	480
Qy	481	AARGRAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELSAQGPVAFHAQRR	540
Db	481	AARGRAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELSAQGPVAFHAQRR	540
Qy	541	QTLQEGGVVLLFSPGNAVALCSEWLDQVSGPGAGHGDFAFRASLSCVLPDLQGRAPGS	600
Db	541	QTLQEGGVVLLFSPGNAVALCSEWLDQVSGPGAGHGDFAFRASLSCVLPDLQGRAPGS	600
Qy	601	YVGACFDRLLHPDAVPALEFRTVPVFTLPSQLPDLFGLAQOPRAPRSRGLQRAEQVSRAL	660
Db	601	YVGACFDRLLHPDAVPALEFRTVPVFTLPSQLPDLFGLAQOPRAPRSRGLQRAEQVSRAL	660
Qy	661	QPALDSYFHPGTPAPGRGVGPGAGDGT 692	
Db	661	QPALDSYFHPGTPAPGRGVGPGAGDGT 692	
RESULT 3			
AAU29322			
ID	AAU29322 standard; Protein; 705 AA.		
AC	AAU29322;		
XX			
DT	18-DEC-2001 (first entry)		
XX			
DE	Human PRO polypeptide sequence #299.		
XX			
KW	PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;		
KW	dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;		
KW	blood; chondrocyte cell; cell proliferation; cell differentiation; colon;		
KW	adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.		
XX			
OS	Homo sapiens.		
PN			
PN	WO200168848-A2.		
XX			
PD	20-SEP-2001.		
XX			
PF	28-FEB-2001; 2001WO-US06520.		
XX			
PR	01-MAR-2000; 2000WO-US05601.		
PR	02-MAR-2000; 2000WO-US05841.		
PR	03-MAR-2000; 2000US-187202P.		
PR	06-MAR-2000; 2000US-186968P.		
PR	14-MAR-2000; 2000US-189320P.		
PR	14-MAR-2000; 2000US-189328P.		
PR	15-MAR-2000; 2000WO-US06884.		
PR	21-MAR-2000; 2000US-190828P.		
PR	21-MAR-2000; 2000US-191007P.		
PR	21-MAR-2000; 2000US-191048P.		
PR	21-MAR-2000; 2000US-191314P.		
PR	28-MAR-2000; 2000US-192655P.		
PR	29-MAR-2000; 2000US-193032P.		
PR	29-MAR-2000; 2000US-193053P.		
PR	30-MAR-2000; 2000WO-US08439.		

PR	04-APR-2000;	2000US-194449P.	PR
PR	04-APR-2000;	2000US-194647P.	PR
PR	11-APR-2000;	2000US-195975P.	PR
PR	11-APR-2000;	2000US-196000P.	PR
PR	11-APR-2000;	2000US-196187P.	PR
PR	11-APR-2000;	2000US-196690P.	PR
PR	11-APR-2000;	2000US-196820P.	PR
PR	18-APR-2000;	2000US-198121P.	PR
PR	18-APR-2000;	2000US-198585P.	PR
PR	25-APR-2000;	2000US-199397P.	PR
PR	25-APR-2000;	2000US-199550P.	PR
PR	25-APR-2000;	2000US-199654P.	PR
PR	03-MAY-2000;	2000US-201516P.	PR
PR	17-MAY-2000;	2000WO-US13705.	PR
PR	22-MAY-2000;	2000WO-US14042.	PR
PR	30-MAY-2000;	2000WO-US14941.	PR
PR	02-JUN-2000;	2000WO-US15264.	PR
PR	05-JUN-2000;	2000US-209832P.	PR
PR	28-JUL-2000;	2000WO-US20710.	PR
PR	22-AUG-2000;	2000US-0644848.	PR
PR	24-AUG-2000;	2000WO-US23328.	PR
PR	08-NOV-2000;	2000WO-US30952.	PR
PR	01-DEC-2000;	2000WO-US32678.	PR
PR	20-DEC-2000;	2000WO-US34956.	PR
XX			
PA	(GETH) GENENTECH INC.		
XX			
PI	Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;		
PI	Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;		
XX			
DR	WPI; 2001-602746/68.		
XX			
DR	N-PSDB; AAS46223.		
XX			
PT	Novel nucleic acids encoding PRO polypeptides, used to diagnose the		
PT	presence of tumours, such as prostate and breast tumours, in mammals and		
PT	to screen for modulators of the compounds -		
XX			
PS	Claim 11; Fig 598; 774pp; English.		
XX			
CC	Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.		
CC	The PRO polypeptides and their associated nucleic acids can be used to		
CC	detect the presence of a tumour in a mammal by comparing the level of		
CC	expression of a PRO polypeptide in a test sample of cells from the animal		
CC	and a control sample of normal cells, whereby a higher level of		
CC	expression in the test sample indicates the presence of a tumour in the		
CC	mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats		
CC	and rabbits but are preferably human. The polypeptides can be used to		
CC	stimulate tumour necrosis factor (TNF) alpha release from human blood,		
CC	when contacted with it. A specific polypeptide can be used to stimulate		
CC	the proliferation or differentiation of chondrocyte cells. The PRO		
CC	proteins can be used to determine the presence of tumours and also		
CC	susceptibility to tumour development, particularly adrenal, lung, colon,		
CC	breast, prostate, rectal, cervical, or liver tumours, in mammalian		
CC	subjects. The oligonucleotide probes specific for the PRO nucleic acids		
CC	can be used for genetic analysis of individuals with genetic disorders.		
XX			
SQ	Sequence	705 AA;	
Query Match			
Best Local Similarity 99.6%; Score 3699.5; DB 22; Length 705;			
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;			
Qy	1	MPVPWFLLSLALGRSPVVLRLERLVGPQDATHCSFGLSCLRLWDSITLCLPGDIVPAGPV 60	
Db	1	MPVPWFLLSLALGRSPVVLRLERLVGPQDATHCSFGLSCLRLWDSITLCLPGDIVPAGPV 60	
Qy	61	LAPTHLQTELVLRCOKETDCDCLLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120	
Db	61	LAPTHLQTELVLRCOKETDCDCLLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120	
Qy	121	LOAQVLSFOAYPTARCVLLEQVPAALVQFGSGVSVYDCFEALGSEVRWTSYQTPR 180	
Db	121	LOAQVLSFOAYPTARCVLLEQVPAALVQFGSGVSVYDCFEALGSEVRWTSYQTPR 180	

CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease, an autoimmune or immune-mediated skin
CC disease, contact dermatitis, an allergic disease e.g. food
CC hypersensitivity, asthma, a transplantation associated disease, or a
CC chronic inflammatory demyelinating polyneuropathy. Treating a
CC degenerative cartilaginous disorder comprises administering a PRO1031 or
CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous
CC examples of the diseases and disorders are given in the specification.
XX
SQ Sequence 705 AA;

Query Match 99.6%; Score 3699.5; DB 22; Length 705;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 MPVPWFLLSALGRSPVVLISLERLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAGPV 60
Db 1 MPVPWFLLSALGRSPVVLISLERLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAGPV 60
QY 61 LAPTHLQTELVLRCOKETDCDCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120
Db 61 LAPTHLQTELVLRCOKETDCDCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120
QY 121 LQAOVVLVSFOAYPTARCVLLEVVQVPAALVQFGQSVGVVYDCFEAALGSEVRINSYTQPR 180
Db 121 LQAOVVLVSFOAYPTARCVLLEVVQVPAALVQFGQSVGVVYDCFEAALGSEVRINSYTQPR 180
QY 181 YEKELNHTQOLPALPWLNVNSADGDNVHLVNSVEQHFGLSLYNQVQGPCKPRHKNLT 240
Db 181 YEKELNHTQOLPALPWLNVNSADGDNVHLVNSVEQHFGLSLYNQVQGPCKPRHKNLT 240
QY 241 GPOIITLNHTDLVPCICIQWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLTLQSWL 300
Db 241 GPOIITLNHTDLVPCICIQWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLTLQSWL 300
QY 301 LDAPCSLPAEALCWAPGDCQPLVPPLSWENVTVDKVFLEPFLKGGHNLQVQVNSSE 360
Db 301 LDAPCSLPAEALCWAPGDCQPLVPPLSWENVTVDKVFLEPFLKGGHNLQVQVNSSE 360
QY 361 KLQLOECLWADSLGPKLDDVLLLETRGPQDNRSICALPEPGCTSLPSKASTRAARLGEYL 420
Db 361 KLQLOECLWADSLGPKLDDVLLLETRGPQDNRSICALPEPGCTSLPSKASTRAARLGEYL 420
QY 421 LQDLQSGQCLOLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLLILLKKDHAK - 479
Db 421 LQDLQSGQCLOLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLLILLKKDHAKG 480
QY 480 -----AAARGRAALLYSADDSGFERLVGALASALCOLPLURVAVDLWSRRELS 527
Db 481 WLRLKQDVRSAGAAARGRAALLYSADDSGFERLVGALASALCOLPLURVAVDLWSRRELS 540
QY 528 AOGPVAMFHAQRRTQLQEGGVVLLFSPGAVALCSWLQDGVSGPAGHGFDAFRASLSC 587
Db 541 AOGPVAMFHAQRRTQLQEGGVVLLFSPGAVALCSWLQDGVSGPAGHGFDAFRASLSC 600
QY 588 VLPDFLQGRAPGSYGACFDRLHDPALFRTVPFTLPSQLPDFLQALQOPRPRSG 647
Db 601 VLPDFLQGRAPGSYGACFDRLHDPALFRTVPFTLPSQLPDFLQALQOPRPRSG 660
QY 648 RLQERAEQVSRALQPALDSYFFHPGTPAPGRGVGPGAGGAGDGT 692
Db 661 RLQERAEQVSRALQPALDSYFFHPGTPAPGRGVGPGAGGAGDGT 705

RESULT 5
AAB87606
ID AAB87606 standard; Protein; 705 AA.
XX
AC AAB87606;

XX 15-MAY-2001 (first entry)
XX Human PRO20040.
XX Human; PRO protein; mapping.
XX Homo sapiens.
XX WO200116318-A2.
XX 08-MAR-2001.
XX 24-AUG-2000; 2000WO-US23328.
XX 01-SEP-1999; 99WO-US20111.
XX 15-SEP-1999; 99WO-US21090.
XX 07-DEC-1999; 99US-0169495.
XX 09-DEC-1999; 99US-0170262.
XX 11-JAN-2000; 2000US-0175481.
XX 18-FEB-2000; 2000WO-US04341.
XX 18-FEB-2000; 2000WO-US04342.
XX 22-FEB-2000; 2000WO-US04414.
XX 01-MAR-2000; 2000WO-US05601.
XX 03-MAR-2000; 2000US-0187202.
XX 25-APR-2000; 2000US-0199397.
XX 22-MAY-2000; 2000WO-US14042.
XX 05-JUN-2000; 2000US-0209832.
XX (GETH) GENENTECH INC.
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2001-183260/18.
XX N-PSDB; AAF92138.
XX Eighty four nucleic acids encoding PRO polypeptides, useful in
XX molecular biology, including use as hybridization probes, and in
XX chromosome and gene mapping.
XX Claim 12; Fig 162; 278pp; English.
XX The present sequence is a human PRO polypeptide (secreted and
XX transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
XX anti-PRO antibodies are useful for preparation of a medicament useful in
XX the treatment of a condition which is responsive to the PRO protein,
XX agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
XX employed as molecular weight markers for protein electrophoresis. The PRO
XX coding sequence has applications in molecular biology, including use as
XX hybridisation probes, and in chromosome and gene mapping.

Sequence 705 AA;

Query Match 99.6%; Score 3699.5; DB 22; Length 705;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 MPVPWFLLSALGRSPVVLISLERLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAGPV 60
Db 1 MPVPWFLLSALGRSPVVLISLERLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAGPV 60
QY 61 LAPTHLQTELVLRCOKETDCDCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120
Db 61 LAPTHLQTELVLRCOKETDCDCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120
QY 121 LQAOVVLVSFOAYPTARCVLLEVVQVPAALVQFGQSVGVVYDCFEAALGSEVRINSYTQPR 180
Db 121 LQAOVVLVSFOAYPTARCVLLEVVQVPAALVQFGQSVGVVYDCFEAALGSEVRINSYTQPR 180
QY 181 YEKELNHTQOLPALPWLNVNSADGDNVHLVNSVEQHFGLSLYNQVQGPCKPRHKNLT 240
Db 181 YEKELNHTQOLPALPWLNVNSADGDNVHLVNSVEQHFGLSLYNQVQGPCKPRHKNLT 240

QY 241 GPOITLNHTDLVPCICIQWVPLEPDSVVRNICPFREDPRAHQNLWQAARLRLTLQSWL 300
DB 241 GPOITLNHTDLVPCICIQWVPLEPDSVVRNICPFREDPRAHQNLWQAARLRLTLQSWL 300
QY 301 LDAPCSLPAAALCWAPGDCQPLVPPLSWENVTVDKVLEFFLLKGHPNLCVQVNSSE 360
DB 301 LDAPCSLPAAALCWAPGDCQPLVPPLSWENVTVDKVLEFFLLKGHPNLCVQVNSSE 360
QY 361 KLQQLQECWLADSLGPKLDDVLLLETRGPQDNRSICALPEPGCTSLPSKASTRAARLGEYL 420
DB 361 KLQQLQECWLADSLGPKLDDVLLLETRGPQDNRSICALPEPGCTSLPSKASTRAARLGEYL 420
QY 421 LQDLSGQCLQWLDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSILILLKKDHAK - 479
DB 421 LQDLSGQCLQWLDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSILILLKKDHAK 480
QY 480 -----AAAGRAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 527
DB 481 WRLLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 540
QY 528 AOGPVAFHQAORRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAGHPHDAFRASLSC 587
DB 541 AOGPVAFHQAORRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAGHPHDAFRASLSC 600
QY 588 VLPDFLQGRAPGSYVACFDRLHHPDAVPALFRTVPVFTLPSQLPDLFALQOQPRAPRSG 647
DB 601 VLPDFLQGRAPGSYVACFDRLHHPDAVPALFRTVPVFTLPSQLPDLFALQOQPRAPRSG 660
QY 648 RLQERAEQVSRAEQVSRALQALDYSYFHPGTPAPGRGVGPGAGGAGDGT 692
DB 661 RLQERAEQVSRAEQVSRALQALDYSYFHPGTPAPGRGVGPGAGGAGDGT 705

RESULT 6

AAAB61884
ID AAB61884 standard; Protein: 705 AA.

AC AAB61884;

DT 08-MAY-2001 (first entry)

XX Chimeric Zcytor14 protein #2.

DE Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
KW antiinflammatory; gene therapy; vaccine.

XX Homo sapiens.

XX WO200104304-A1.

XX 18-JAN-2001.

XX 30-JUN-2000; 2000WO-US18383.

XX 07-JUL-1999; 99US-0348854.

XX (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, Burkhead SK, Pownder SL;

XX WPI; 2001-112618/12.

PT New polypeptide encoding a human cytokine receptor Zcytor14, for
PT treating inflammation e.g. rheumatoid arthritis -

XX Claim 2; Page 105-107; 112pp; English.

XX The invention provides a new human cytokine receptor designated Zcytor14.
CC Zcytor14 can be expressed by standard recombinant methodology. The
CC encoding nucleic acid is useful for detecting the expression of a
CC Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be
CC used to screen biological samples in vitro for the presence of Zcytor14.

CC Proteins, polypeptides and peptides having Zcytor14 activity can be
CC administered to a subject who lacks an adequate amount of this
CC polypeptide, for treating inflammation and conditions such as rheumatoid
CC arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14
CC antibodies) can be used to treat a subject who produces an excess of
CC Zcytor14. Zcytor14 nucleotide sequences can also be used to provide
CC Zcytor14 to a subject. The present sequence represents a chimeric
XX Zcytor14 protein.

SQ Sequence 705 AA;

Query Match 99.6%; Score 3699.5; DB 22; Length 705;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 MPVPWFLLSALGRSPVLSLERLVGPQDATHCSPGLSRLWDSIDLCLPGDIVPAGPV 60
DB 1 MPVPWFLLSALGRSPVLSLERLVGPQDATHCSPGLSRLWDSIDLCLPGDIVPAGPV 60
QY 61 LAPTHLQTELVLRCOKETDCDCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120
DB 61 LAPTHLQTELVLRCOKETDCDCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120
QY 121 LQAQVVLSPQAYPTARCVLLEQVPAALYFGQSVGVVYDCFEAALGSEVRWISYTPR 180
DB 121 LQAQVVLSPQAYPTARCVLLEQVPAALYFGQSVGVVYDCFEAALGSEVRWISYTPR 180
QY 181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEQHFGLSLYNVQVQPPKRWKNT 240
DB 181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEQHFGLSLYNVQVQPPKRWKNT 240
QY 241 GPOIITLNHTDLVPCICIQWVPLEPDSVVRNICPFREDPRAHQNLWQAARLRLTLQSWL 300
DB 241 GPOIITLNHTDLVPCICIQWVPLEPDSVVRNICPFREDPRAHQNLWQAARLRLTLQSWL 300
QY 301 LDAPCSLPAAALCWAPGDCQPLVPPLSWENVTVDKVLEFFLLKGHPNLCVQVNSSE 360
DB 301 LDAPCSLPAAALCWAPGDCQPLVPPLSWENVTVDKVLEFFLLKGHPNLCVQVNSSE 360
QY 361 KLQQLQECWLADSLGPKLDDVLLLETRGPQDNRSICALPEPGCTSLPSKASTRAARLGEYL 420
DB 361 KLQQLQECWLADSLGPKLDDVLLLETRGPQDNRSICALPEPGCTSLPSKASTRAARLGEYL 420
QY 421 LQDLSGQCLQWLDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSILILLKKDHAK - 479
DB 421 LQDLSGQCLQWLDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSILILLKKDHAK 480
QY 480 -----AAAGRAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 527
DB 481 WRLLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 540
QY 528 AOGPVAFHQAORRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAGHPHDAFRASLSC 587
DB 541 AOGPVAFHQAORRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAGHPHDAFRASLSC 600
QY 588 VLPDFLQGRAPGSYVACFDRLHHPDAVPALFRTVPVFTLPSQLPDLFALQOQPRAPRSG 647
DB 601 VLPDFLQGRAPGSYVACFDRLHHPDAVPALFRTVPVFTLPSQLPDLFALQOQPRAPRSG 660
QY 648 RLQERAEQVSRAEQVSRALQALDYSYFHPGTPAPGRGVGPGAGGAGDGT 692
DB 661 RLQERAEQVSRAEQVSRALQALDYSYFHPGTPAPGRGVGPGAGGAGDGT 705

RESULT 7

ABB95604
ID ABB95604 standard; Protein: 705 AA.

XX ABB95604;

XX 19-JUL-2002 (first entry)

DE Human angiogenesis related protein PRO20040 SEQ ID NO: 364.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiac; cytoskeletal; antiangiogenic; hypotensive; vulnerary;
XX antiarteriosclerotic.

OS Homo sapiens.
XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 25-JUL-2000; 2000US-220664P.

XX 28-JUL-2000; 2000WO-US20710.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-0643657.

XX 23-AUG-2000; 2000WO-US223522.

XX 24-AUG-2000; 2000WO-US22328.

XX 07-SEP-2000; 2000US-230978P.

XX 15-SEP-2000; 2000US-000000P.

XX 18-SEP-2000; 2000US-0664610.

XX 18-SEP-2000; 2000US-0664610.

XX 24-OCT-2000; 2000US-0665350.

XX 08-NOV-2000; 2000US-0709238.

XX 08-NOV-2000; 2000WO-US30952.

XX 10-NOV-2000; 2000WO-US30873.

XX 01-DEC-2000; 2000WO-US32678.

XX 20-DEC-2000; 2000US-0747259.

XX 20-DEC-2000; 2000WO-US34956.

XX 22-JAN-2001; 2001US-0767609.

XX 28-FEB-2001; 2001US-0796498.

XX 28-FEB-2001; 2001WO-US05520.

XX 01-MAR-2001; 2001WO-US06666.

XX 09-MAR-2001; 2001US-0802706.

XX 14-MAR-2001; 2001US-0808689.

XX 22-MAR-2001; 2001US-0816744.

XX 05-APR-2001; 2001US-0828366.

XX 10-MAY-2001; 2001US-0854208.

XX 10-MAY-2001; 2001US-0854280.

XX 25-MAY-2001; 2001US-0866028.

XX 25-MAY-2001; 2001US-0866034.

XX 25-MAY-2001; 2001WO-US17092.

XX 30-MAY-2001; 2001US-0870574.

XX 30-MAY-2001; 2001WO-US17443.

XX 01-JUN-2001; 2001WO-US17800.

XX 20-JUN-2001; 2001WO-US19692.

XX 28-JUN-2001; 2001WO-US00000.

XX (GETH) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODORSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (PANJ/) PAN J.

PA (PAON/) PAONI N F.

PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX

DR WPI: 2002-171999/22.

XX N-PSDB; ABL95742.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

XX infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 364; 567pp; English.

XX The present invention provides the protein and coding sequences of human

CC PRO proteins. These are useful for treating or diagnosing a

CC cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,

CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

XX healing. The present sequence is a PRO protein of the invention.

XX Sequence 705 AA;

Query Match 99.6%; Score 3699.5; DB 23; Length 705;

Best Local Similarity 98.2%; Pred. No. 0;

Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 MPVPWFLLSLALGRSPVLSRLERLVGPQDATHCSPGLSRLWDSILCLPGDIVPAGPV 60

Db 1 MPVPWFLLSLALGRSPVLSRLERLVGPQDATHCSPGLSRLWDSILCLPGDIVPAGPV 60

Qy 61 LAPTHLOTQLVLRCKETDCDCLRLVAVHLVHGHWEPEDEKFGGAADSGVEEPRNAS 120

Db 61 LAPTHLOTQLVLRCKETDCDCLRLVAVHLVHGHWEPEDEKFGGAADSGVEEPRNAS 120

Qy 121 LQAQVWLSFOAYPTARCVLLEVOVPAALVQFGQSVGVYVDCFEALGSEVRWSTQPR 180

Db 121 LQAQVWLSFOAYPTARCVLLEVOVPAALVQFGQSVGVYVDCFEALGSEVRWSTQPR 180

Qy 181 YEKELNHTQQLPALPMLNVSDGDNVHLVNVSEHQHGLSLYVQVQVQPPRHKNT 240

Db 181 YEKELNHTQQLPALPMLNVSDGDNVHLVNVSEHQHGLSLYVQVQVQPPRHKNT 240

Qy 241 GPQIITLNHTDLVPCICIQVWPLEPDSVTRTNCPPREDPRAHQNLMQARLLTLQSWL 300

Db 241 GPQIITLNHTDLVPCICIQVWPLEPDSVTRTNCPPREDPRAHQNLMQARLLTLQSWL 300

Qy 301 LDAPCSLPAEALCWRAFGDPCQPLVPPLSWENTVDKLEFLLKGNPLNCVQVNSSE 360

Db 301 LDAPCSLPAEALCWRAFGDPCQPLVPPLSWENTVDKLEFLLKGNPLNCVQVNSSE 360

Qy 361 KLQEQECLWADSLGPKDDVLLLETRGPQDNRSCLALEPSGCTSLPSKASTRAARLGEYL 420

Db 361 KLQEQECLWADSLGPKDDVLLLETRGPQDNRSCLALEPSGCTSLPSKASTRAARLGEYL 420

Qy 421 LQDLSGQCLQWLWDDDLGALWACPMKYIHKRWALVWLACLLFAAALSILLLKKDHAK - 479

Db 421 LQDLSGQCLQWLWDDDLGALWACPMKYIHKRWALVWLACLLFAAALSILLLKKDHAK 480

Qy 480 -----AAARGRAALLLYSADSGFERLVGALASALCQLPLRVAVDLWSRRELS 527

Db 481 WLRLLKQDVRSAAAARGRAALLLYSADSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy 528 AOGPVANFHAORROTLOEGGVVWLLFSPCAVALCSEWLDQGVSGCAHGPDAFRASLSC 587

Db 541 AOGPVANFHAORROTLOEGGVVWLLFSPCAVALCSEWLDQGVSGCAHGPDAFRASLSC 600

Qy 588 VLPDFLQGRAPGSYVACFDRLHHPDAVPALFRTVPVFTLPSQLPDFLQALQOQPRAPRS 647

Db 601 VLPDFLQGRAPGSYVACFDRLHHPDAVPALFRTVPVFTLPSQLPDFLQALQOQPRAPRS 660

Qy 648 RLQRAEQVSRALQALDSYFHPFGTTPAGRGVGPAGGAGDGT 692

Db 661 RLQRAEQVSRALQALDSYFHPFGTTPAGRGVGPAGGAGDGT 705

RESULT 8
 ABB84998
 ID ABB84998 standard; Protein; 705 AA.
 XX AC ABB84998;
 XX DT 16-MAY-2002 (first entry)
 XX DE Human PRO20040 protein sequence SEQ ID NO:364.
 XX KW Human; angiogenesis; cardiast; cytostatic; antiangiogenic; hypotensive;
 KW KW vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW KW age-related macular degeneration; arterial stenosis; angina;
 KW KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW KW wound healing; chromosome mapping; gene mapping.
 XX OS Homo sapiens.
 XX WO200200690-A2.
 XX PD 03-JAN-2002.
 XX PF 20-JUN-2001; 2001WO-US19692.
 XX PR 23-JUN-2000; 2000US-213637P.
 XX PR 20-JUL-2000; 2000US-219556P.
 XX PR 25-JUL-2000; 2000US-220624P.
 XX PR 25-JUL-2000; 2000US-220664P.
 XX PR 28-JUL-2000; 2000WO-US20710.
 XX PR 02-AUG-2000; 2000US-222695P.
 XX PR 17-AUG-2000; 2000US-0643657.
 XX PR 23-AUG-2000; 2000WO-US23522.
 XX PR 24-AUG-2000; 2000WO-US23328.
 XX PR 07-SEP-2000; 2000US-230978P.
 XX PR 18-SEP-2000; 2000US-0664610.
 XX PR 18-SEP-2000; 2000US-0665350.
 XX PR 24-OCT-2000; 2000US-242922P.
 XX PR 08-NOV-2000; 2000US-0709238.
 XX PR 08-NOV-2000; 2000WO-US30952.
 XX PR 10-NOV-2000; 2000WO-US30873.
 XX PR 01-DEC-2000; 2000WO-US32678.
 XX PR 20-DEC-2000; 2000US-0747259.
 XX PR 20-DEC-2000; 2000WO-US34956.
 XX PR 22-JAN-2001; 2001US-0767609.
 XX PR 28-FEB-2001; 2001US-0796498.
 XX PR 01-MAR-2001; 2001WO-US06520.
 XX PR 09-MAR-2001; 2001US-0802706.
 XX PR 14-MAR-2001; 2001US-0808689.
 XX PR 22-MAR-2001; 2001US-0816744.
 XX PR 05-APR-2001; 2001US-0828366.
 XX PR 10-MAY-2001; 2001US-0854208.
 XX PR 10-MAY-2001; 2001US-0854208.
 XX PR 25-MAY-2001; 2001US-0866028.
 XX PR 25-MAY-2001; 2001US-0866034.
 XX PR 25-MAY-2001; 2001WO-US17092.
 XX PR 30-MAY-2001; 2001US-0870574.
 XX PR 30-MAY-2001; 2001WO-US17443.
 XX PR 01-JUN-2001; 2001WO-US17800.
 XX (GETH) GENENTECH INC.
 XX PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 XX PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 XX PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI: 2002-090516/12.
 XX DR N-PSDB; ABL88253.
 XX PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,

useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
 Claim 11; Fig 364; 565pp; English.
 ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis, angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.
 SQ Sequence 705 AA;
 Query Match 99.6%; Score 3699.5; DB 23; Length 705;
 Best Local Similarity 98.2%; Pred. No. 0;
 Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
 QY 1 MPVPWFLSLALGRSPVLSLERLVGPQDATHCSPLGSLCRLWDSILCLPGDIVPAGPV 60
 Db 1 MPVPWFLSLALGRSPVLSLERLVGPQDATHCSPLGSLCRLWDSILCLPGDIVPAGPV 60
 QY 61 LAPHLOTELVLRCQKEDCDLCLRVAVHLAVHGHWEPEDEEKGGAADSGVEPRNAS 120
 Db 61 LAPHLOTELVLRCQKEDCDLCLRVAVHLAVHGHWEPEDEEKGGAADSGVEPRNAS 120
 QY 121 LQOVVLSFOAYPTARCVLLEVQVPAALVQFGSVGVVYDCFEAALGSEVRINWYTOPR 180
 Db 121 LQOVVLSFOAYPTARCVLLEVQVPAALVQFGSVGVVYDCFEAALGSEVRINWYTOPR 180
 QY 181 YEKELNHTQQLPALPWLNVSDAGDNVHLVNVSEOHFGLSLYWNVOGPKPRWKKNL 240
 Db 181 YEKELNHTQQLPALPWLNVSDAGDNVHLVNVSEOHFGLSLYWNVOGPKPRWKKNL 240
 QY 241 GPQIITLHNTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLLTLQSWL 300
 Db 241 GPQIITLHNTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLLTLQSWL 300
 QY 301 LDAPCSLPAAALCWRAAGDPCQPLVPPLSWENVTVDKLEFFLLKHPNLCVQVNSSE 360
 Db 301 LDAPCSLPAAALCWRAAGDPCQPLVPPLSWENVTVDKLEFFLLKHPNLCVQVNSSE 360
 QY 361 KLQLOECLWADSLGPKLDDVLLLETRGPQDNRSILCALEPSGCTSLPSKASTRAARLGEYL 420
 Db 361 KLQLOECLWADSLGPKLDDVLLLETRGPQDNRSILCALEPSGCTSLPSKASTRAARLGEYL 420
 QY 421 LODLSGQCILQWLDDDLGALWACPMKDYIHKRWALVWLACLLFAAALSILLKKDKAK - 479
 Db 421 LODLSGQCILQWLDDDLGALWACPMKDYIHKRWALVWLACLLFAAALSILLKKDKAK 480
 QY 480 -----AAAGRAALLYSADDSGFERLVGALASALCOLPLURVAVDLWSRRELS 527
 Db 481 WLRLKQDVRSGAARAAALLYSADDSGFERLVGALASALCOLPLURVAVDLWSRRELS 540
 QY 528 AOGPVAFWFAHQRROTLEQGGVVLLFSPGVALCSEHLDQVSGPGAGHPDFAFRSLSC 587
 Db 541 AOGPVAFWFAHQRROTLEQGGVVLLFSPGVALCSEHLDQVSGPGAGHPDFAFRSLSC 600
 QY 588 VLPDFLQGRAPGSYVGACFDRLHDPALFRTVPVFTLPSPQLPDFLQALQOPRPSG 647
 Db 601 VLPDFLQGRAPGSYVGACFDRLHDPALFRTVPVFTLPSPQLPDFLQALQOPRPSG 660
 QY 648 RLQERAEQVSRALQPALDSYFHPPTAPGGRGVGPGAGGAGDGT 692
 Db 661 RLQERAEQVSRALQPALDSYFHPPTAPGGRGVGPGAGGAGDGT 705

RESULT 9	
AAU98792	AAU98792 standard; Protein; 705 AA.
XX	
AC	AAU98792;
XX	
DT	24-SEP-2002 (first entry)
XX	
DE	Human interleukin 17 receptor like protein, splice variant protein #11.
XX	
KW	Human; receptor; Interleukin 17 receptor-like protein; IL-17RL;
KW	Chondroleukin; bone degradation; cartilage degradation; gene therapy;
KW	chromosome 3p25.3-3p24.1; rheumatoid arthritis; multiple sclerosis;
KW	allergic skin immune response; organ transplant rejection; cytokine;
KW	osteopathic; antirheumatic; antiarthritic; relapsing polychondritis;
KW	seronegative spondyloarthopathy; bone morphogenetic protein;
KW	splice variant.
XX	
OS	Homo sapiens.
XX	
PN	WO200238764-A2.
XX	
PD	16-MAY-2002.
XX	
PF	13-NOV-2001; 2001WO-US43855.
XX	
PR	10-NOV-2000; 2000US-247134P.
PR	23-FEB-2001; 2001US-271197P.
PR	12-OCT-2001; 2001US-328904P.
XX	
XX	(REGC) UNIV CALIFORNIA.
PA	
XX	
PI	Haudenschild D, Rose L, Moseley T, Reddi AH;
XX	
DR	WPI: 2002-508211/54.
DR	N-PSDB; ABK86558.
XX	
PT	Interleukin-17 receptor-like polypeptide useful for the manufacture of
PT	a medicament to modulate cartilage or bone growth in a mammal
XX	
PS	Claim 1; Page 87; 108pp; English.
XX	
CC	The invention relates to an interleukin-17 receptor-like (IL-17RL)
CC	polypeptide, with 85% or greater sequence identity to a polypeptide with
CC	a sequence appearing as AAU98781-AAU98792, where IL-17RL binds
CC	to an IL-17 selected from IL-17A, IL-17B, IL-17C, IL-17E and IL-17F.
CC	Also included are IL-17RL polynucleotides, antibodies, expression
CC	cassettes, transgenic host cells, a method of determining the
CC	aggressiveness of a prostate cancer cell, by determining the presence or
CC	absence in the cell of a group of IL-17RL (where the determination that
CC	the group is absent in the cell indicates that the cancer is more
CC	aggressive than a like cell in which the group is present) and a
CC	mammalian cell comprising a polynucleotide encoding an IL-17B antagonist,
CC	where the cell is selected from chondrocyte, synovioocyte, and mesenchymal
CC	stem cell. IL-17RL or the polynucleotide is useful for the manufacture of
CC	a medicament to modulate cartilage or bone growth in a mammal. The
CC	polynucleotide is useful for the manufacture of a medicament to restore
CC	androgen-responsiveness to a prostate cancer cell. IL-17RL is useful for
CC	decreasing catabolic activity in bone or cartilage in a mammal. IL-17RL
CC	is useful for inhibiting ossification or calcification in a mammal
CC	suffering from pathological ossification or calcification, for diagnosing
CC	a cartilage degenerative disorder in a mammal, for inhibiting the rate of
CC	proteoglycan synthesis by a chondrocyte in culture, and for the
CC	manufacture of a medicament to potentiate the activity of a bone
CC	morphogenetic protein in a mammal. An IL-17RL antagonist is useful
CC	for treating a bone or cartilage pathology such as a degenerative
CC	cartilage disorder selected from osteoarthritis, rheumatoid arthritis,
CC	relapsing polychondritis, seronegative spondyloarthropathies, multiple
CC	sclerosis, allergic skin immune response and organ transplant rejection.
CC	IL-17RL is particularly a receptor for IL-17B (Chondroleukin, a
CC	proinflammatory cytokine). The gene for IL-17B is located on

KW seronegative spondyloarthropathy; bone morphogenetic protein.

XX Homo sapiens.

PN WO200238764-A2.

PD 16-MAY-2002.

XX 13-NOV-2001; 2001WO-US43855.

XX 10-NOV-2000; 2000US-2471134P.

PR 23-FEB-2001; 2001US-271197P.

PR 12-OCT-2001; 2001US-328904P.

XX (REGC) UNIV CALIFORNIA.

XX Haudenschild D, Rose L, Moseley T, Reddi AH;

XX WPI; 2002-508211/54.

DR N-PSDB; ABK86547.

XX Interleukin-17 receptor-like polypeptide useful for the manufacture of

XX a medicament to modulate cartilage or bone growth in a mammal

XX Claim 1; Fig 2; 108pp; English.

XX The invention relates to an interleukin-17 receptor-like (IL-17RL) polypeptide, with 85% or greater sequence identity to a polypeptide with a sequence appearing as AAU98781-AAU98792, where IL-17RL binds to an IL-17 selected from IL-17A, IL-17B, IL-17C, IL-17E and IL-17F. Also included are IL-17RL polynucleotides, antibodies, expression cassettes, transgenic host cells, a method of determining the aggressiveness of a prostate cancer cell, by determining the presence or absence in the cell of a group of IL-17RL (where the determination that the group is absent in the cell indicates that the cancer is more aggressive than a like cell in which the group is present) and a mammalian cell comprising a polynucleotide encoding an IL-17B antagonist, where the cell is selected from chondrocyte, synovioocyte, and mesenchymal stem cell. IL-17RL or the polynucleotide is useful for the manufacture of a medicament to modulate cartilage or bone growth in a mammal. The polynucleotide is useful for the manufacture of a medicament to restore androgen-responsiveness to a prostate cancer cell. IL-17RL is useful for decreasing catabolic activity in bone or cartilage in a mammal. IL-17RL is useful for inhibiting ossification or calcification in a mammal suffering from pathological ossification or calcification, for diagnosing a cartilage degenerative disorder in a mammal, for inhibiting the rate of proteoglycan synthesis by a chondrocyte in culture, and for the manufacture of a medicament to potentiate the activity of a bone morphogenetic protein in a mammal. An IL-17RL antagonist is useful for treating a bone or cartilage pathology such as a degenerative cartilage disorder selected from osteoarthritis, rheumatoid arthritis, relapsing polychondritis, seronegative spondyloarthropathies, multiple sclerosis, allergic skin immune response and organ transplant rejection. IL-17RL is particularly a receptor for IL-17B (chondroleukin, a proinflammatory cytokine). The gene for IL-17RL is located on chromosome 3p25.3-3p24.1. The present sequence is the full length sequence for IL-17RL.

XX Sequence 720 AA;

Query Match 98.3%; Score 3654; DB 23; Length 720;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 688; Conservative 0; Mismatches 4; Indels 28; Gaps 2;

QY 1 MPVPWFLLSLALGRSPVVLISLERLVGPQDATHCSPLGSLRLWDSIDILCLPGDIVPAPGPV 60

Db 1 MPVPWFLLSLALGRSPVVLISLERLVGPQDATHCSPLGSLRLWDSIDILCLPGDIVPAPGPV 60

QY 61 LAPHLOTELVLRCQKETDCDCLCLRAVHLAVHGWHEEPEDEKFGGAADSGVEEPRNAS 120

Db 61 LAPHLOTELVLRCQKETDCDCLCLRAVHLAVHGWHEEPEDEKFGGAADSGVEEPRNAS 120

QY 121 LQAQWLSFQAYPTARCVLLEQVPAALVQFGQSGSVVYDCFEAALGSEVRIMSWTQPR 180

Db 121 LQAQWLSFQAYPTARCVLLEQVPAALVQFGQSGSVVYDCFEAALGSEVRIMSWTQPR 180
QY 181 YEKELNHTQOLP-----ALPWLNVSDGDNVHLVNLVYSEHQHFGLSLYWN 225
Db 181 YEKELNHTQOLPDCRGLEVNWSIPSCWALPWLNVSDGDNVHLVNLVYSEHQHFGLSLYWN 240
QY 226 QVQGGPKPRWHKNTLGPQIITLNHTDLVPCLCIQVWPLEPDSVTRNTICPREDPRAHNL 285
Db 241 QVQGGPKPRWHKNTLGPQIITLNHTDLVPCLCIQVWPLEPDSVTRNTICPREDPRAHNL 300
QY 286 WQAARLRLTLQSWLLDAPCSLPAEALCWRAFGGPPCOPPLVPPLSWENVTVDKVLFEPL 345
Db 301 WQAARLRLTLQSWLLDAPCSLPAEALCWRAFGGPPCOPPLVPPLSWENVTVDKVLFEPL 360
QY 346 LKGHPNLCVQVNSSEKILQLOECLWADSLGPKDDVLLLETRGPDNRSCLCALPSPGCTSL 405
Db 361 LKGHPNLCVQVNSSEKILQLOECLRADSLGPKDDVLLLETRGPDNRSCLCALPSPGCTSL 420
QY 406 PSKASTRAARLGEYLQDLOSQCLOLWDDDLGALWACPMKYIHKRWALVWLACLLFAA 465
Db 421 PSKASTRAARLGEYLQDLOSQCLOLWDDDLGALWACPMKYIHKRWALVWLACLLFAA 480
QY 466 ALSLLILLKKDHAK-----AAARGPAAALLYSADDSGFERLVGALASALCQL 512
Db 481 ALSLLILLKKDHAKWMLRLKQDVRSGAAARGPAAALLYSADDSGFERLVGALASALCQL 540
QY 513 PLRVAVDLWSRRELSAQGPVAVWFHAQRROTLOEGGVVLLFSPGAVALCSEWLQDGVSGP 572
Db 541 PLRVAVDLWSRRELSAQGPVAVWFHAQRROTLOEGGVVLLFSPGAVALCSEWLQDGVSGP 600
QY 573 GAHPHDAFRASLSCVLPDLQGRAPGSYVGACFDRLHHPDAVPALFRTVPVFTLPSQLP 632
Db 601 GAHPHDAFRASLSCVLPDLQGRAPGSYVGACFDRLHHPDAVPALFRTVPVFTLPSQLP 660
QY 633 DFLGALQPRAPRSRQLQERAEQVSRALQPALDSYFHPHFGTAPAGRGVFGAGPGAGDGT 692
Db 661 DFLGALQPRAPRSRQLQERAEQVSRALQPALDSYFHPHFGTAPAGRGVFGAGPGAGDGT 720

RESULT 11
AAB61885
ID AAB61885 standard; Protein; 675 AA.
XX AAB61885;
XX 08-MAY-2001 (first entry)
XX Chimeric Zcytor14 protein #3.
XX Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
XX antiinflammatory; gene therapy; vaccine.
XX Homo sapiens.
XX WO200104304-A1.
XX 18-JAN-2001.
XX 30-JUN-2000; 2000WO-US18383.
XX 07-JUL-1999; 99US-0348854.
XX (ZYMO) ZYMOGENETICS INC.
XX Presnell SR, Burkhead SK, Pownder SL;
XX WPI; 2001-112618/12.
XX New polypeptide encoding a human cytokine receptor Zcytor14, for
XX treating inflammation e.g. rheumatoid arthritis -
XX Claim 2; Page 107-109; 112pp; English.


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XX The invention provides a new human cytokine receptor designated zcytor14.
CC zcytor14 can be expressed by standard recombinant methodology. The
CC encoding nucleic acid is useful for detecting the expression of a
CC zcytor14 gene in a biological sample. Anti-zcytor14 antibodies can be
CC used to screen biological samples in vitro for the presence of zcytor14.
CC Proteins, polypeptides and peptides having zcytor14 activity can be
CC administered to a subject who lacks an adequate amount of this
CC polypeptide, for treating inflammation and conditions such as rheumatoid
CC arthritis. In contrast, zcytor14 antagonists (e.g. anti-zcytor14
CC antibodies) can be used to treat a subject who produces an excess of
CC zcytor14. zcytor14 nucleotide sequences can also be used to provide
CC zcytor14 to a subject. The present sequence represents a chimeric
CC zcytor14 protein.
XX
SQ Sequence 675 AA;

Query Match          97.0%; Score 3604.5; DB 22; Length 675;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 675; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

QY 1 MPVPWFLLSLALGRSPVLSLERLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAGPV 60
DQ 1 MPVPWFLLSLALGRSPVLSLERLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAGPV 60
QY 61 LAPTHLOTELVLRCOKETDCDCLRLRVAVHLAVHGHWEPEDEKFGGAADSGVEEPRNAS 120
DQ 61 LAPTHLOTELVLRCOKETDCDCLRLRVAVHLAVHGHWEPEDEKFGGAADSGVEEPRNAS 120
QY 121 LQAQVVLVSFOAYPTARCVLLEVVQVPAALVQFGSGSVVYDCFEAALGSEVRWISYTOPR 180
DQ 121 LQAQVVLVSFOAYPTARCVLLEVVQVPAALVQFGSGSVVYDCFEAALGSEVRWISYTOPR 180
QY 181 YEKELNHTQOLPALPWLNVNSADGDNVHLVNVSEQHFGLSLYNVQVGGPPKPRWHKNT 240
DQ 181 YEKELNHTQOLPALPWLNVNSADGDNVHLVNVSEQHFGLSLYNVQVGGPPKPRWHKNT 240
QY 241 GPQIITLNHTDLVPCICIQWVPLEPDSVRTNICPFREDPRAHQNLWQAARLLTLTQSWL 300
DQ 241 GPQIITLNHTDLVPCICIQWVPLEPDSVRTNICPFREDPRAHQNLWQAARLLTLTQSWL 300
QY 301 LDAPCSLPAEALCWRAFGDPCQPLVPLSWENVTVDKVLFFLLKGHPNLCVQVNSSE 360
DQ 301 LDAPCSLPAEALCWRAFGDPCQPLVPLSWENVTVDKVLFFLLKGHPNLCVQVNSSE 360
QY 361 KLQLOECLWADSLGPKLDDVLLLETGPDQNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
DQ 361 KLQLOECLWADSLGPKLDDVLLLETGPDQNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
QY 421 LQDLSGGCQLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLLILLKKDKHAKA 480
DQ 421 LQDLSGGCQLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLLILLKKDKHAKA 480
QY 481 AARGRAALLLYSADDSGFERLVALSALCOLPLRVAVDLWSRRELSAQGPVAFHQAQR 540
DQ 481 AARGRAALLLYSADDSGFERLVALSALCOLPLRVAVDLWSRRELSAQGPVAFHQAQR 540
QY 541 QTLQEGGVVLLFSPCAVALCSEWLQDYGSGPCAHGPHDAFRASLSCVLPDFLQGRAPGS 600
DQ 541 QTLQEGGVVLLFSPCAVALCSEWLQDYGSGPCAHGPHDAFRASLSCVLPDFLQGRAPGS 600
QY 583 YVGAFCFDRLLHPDAPALPRTVPVFTLPQSLPDFLQALQOPRAPRSGRLQERAEQVSRL 660
DQ 583 YVGAFCFDRLLHPDAPALPRTVPVFTLPQSLPDFLQALQOPRAPRSGRLQERAEQVSRL 660
QY 661 QPALDSYFHPGCTPAPGRGVGFCAGPGAGDGT 692
DQ 661 QPALDSYFHPGCTPAPGRGVGFCAGPGAGDGT 692
QY 692 QPALDSYFHPGCTPAPGRGVGFCAGPGAGDGT 692
DQ 692 QPALDSYFHPGCTPAPGRGVGFCAGPGAGDGT 692

RESULT 12
AAB61883
ID AAB61883 standard; Protein; 688 AA.
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XX AAB61883;
XX 08-MAY-2001 (first entry)
XX Chimeric zcytor14 protein #1.
XX Cytokine receptor; zcytor14; human; inflammation; rheumatoid arthritis;
XX antiinflammatory; gene therapy; vaccine.
XX Homo sapiens.
XX WO200104304-A1.
XX 18-JAN-2001.
XX 30-JUN-2000; 2000WO-US18383.
XX 07-JUL-1999; 99US-0348854.
XX (ZYMO ) ZYMOGENETICS INC.
XX Presnell SR, Burkhead SK, Powder SL;
XX WPI; 2001-112618/12.
XX New polypeptide encoding a human cytokine receptor zcytor14, for
XX treating inflammation e.g. rheumatoid arthritis -
XX Claim 2; Page 102-104; 112pp; English.
XX The invention provides a new human cytokine receptor designated zcytor14.
XX zcytor14 can be expressed by standard recombinant methodology. The
XX encoding nucleic acid is useful for detecting the expression of a
XX zcytor14 gene in a biological sample. Anti-zcytor14 antibodies can be
XX used to screen biological samples in vitro for the presence of zcytor14.
XX proteins, polypeptides and peptides having zcytor14 activity can be
XX administered to a subject who lacks an adequate amount of this
XX polypeptide, for treating inflammation and conditions such as rheumatoid
XX arthritis. In contrast, zcytor14 antagonists (e.g. anti-zcytor14
XX antibodies) can be used to treat a subject who produces an excess of
XX zcytor14. zcytor14 nucleotide sequences can also be used to provide
XX zcytor14 to a subject. The present sequence represents a chimeric
XX zcytor14 protein.
XX
SQ Sequence 688 AA;

Query Match          96.6%; Score 3588; DB 22; Length 688;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 675; Conservative 0; Mismatches 0; Indels 30; Gaps 2;

QY 1 MPVPWFLLSLALGRSPVLSLERLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAGPV 60
DQ 1 MPVPWFLLSLALGRSPVLSLERLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAGPV 60
QY 61 LAPTHLOTELVLRCOKETDCDCLRLRVAVHLAVHGHWEPEDEKFGGAADSGVEEPRNAS 120
DQ 61 LAPTHLOTELVLRCOKETDCDCLRLRVAVHLAVHGHWEPEDEKFGGAADSGVEEPRNAS 120
QY 121 LQAQVVLVSFOAYPTARCVLLEVVQVPAALVQFGSGSVVYDCFEAALGSEVRWISYTOPR 180
DQ 121 LQAQVVLVSFOAYPTARCVLLEVVQVPAALVQFGSGSVVYDCFEAALGSEVRWISYTOPR 180
QY 181 YEKELNHTQOLPALPWLNVNSADGDNVHLVNVSEQHFGLSLYNVQVGGPPKPRWHKNT 240
DQ 181 YEKELNHTQOLPALPWLNVNSADGDNVHLVNVSEQHFGLSLYNVQVGGPPKPRWHKNT 240
QY 241 GPQIITLNHTDLVPCICIQWVPLEPDSVRTNICPFREDPRAHQNLWQAARLLTLTQSWL 300
DQ 241 GPQIITLNHTDLVPCICIQWVPLEPDSVRTNICPFREDPRAHQNLWQAARLLTLTQSWL 300
QY 301 LDAPCSLPAEALCWRAFGDPCQPLVPLSWENVTVDKVLFFLLKGHPNLCVQVNSSE 360
DQ 301 LDAPCSLPAEALCWRAFGDPCQPLVPLSWENVTVDKVLFFLLKGHPNLCVQVNSSE 360
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Db 301 LDAPCSLPAAALCWAPGDPQCPPLVPLSWENVTVD-----VNSSE 343
QY 361 KLOQECWLWADSLGPKDDVLLLETRGPQDNRSICALPSGCTSLPSKASTRAARLGEYL 420
Db 344 KLOQECWLWADSLGPKDDVLLLETRGPQDNRSICALPSGCTSLPSKASTRAARLGEYL 403
QY 421 LQDLSGQCLQWDDDLGALWACPMKYIHKRWALVWLACLLFAAALSLLLLKKDHAK- 479
Db 404 LQDLSGQCLQWDDDLGALWACPMKYIHKRWALVWLACLLFAAALSLLLLKKDHAKG 463
QY 480 -----AAARGRAALLYSDSGFERLVGALASALCOLPRAVAVDLMSRRELS 527
Db 464 WLRLKQDVRSAGAAAGRAALLYSDSGFERLVGALASALCOLPRAVAVDLMSRRELS 523
QY 528 ACPVAFWFAHQRTQLQEGGVVLLFSPGAVALCSEWLQDGVSPGAGHPHDAFRASLSC 587
Db 524 ACPVAFWFAHQRTQLQEGGVVLLFSPGAVALCSEWLQDGVSPGAGHPHDAFRASLSC 583
QY 588 VLPDFLQGRAPGSYGACFDRLLHPDAVPALFRTVPVFTLPSQLPDLFGALQQPRAPRS 647
Db 584 VLPDFLQGRAPGSYGACFDRLLHPDAVPALFRTVPVFTLPSQLPDLFGALQQPRAPRS 643
QY 648 RLQERAEQVSRALQPALDSYFHPGTPAPGRGVGPGAGCGAGDGT 692
Db 644 RLQERAEQVSRALQPALDSYFHPGTPAPGRGVGPGAGCGAGDGT 688

RESULT 13
AAU98791
ID AAU98791 standard; Protein; 703 AA.
XX AC AAU98791;
XX DT
XX DE Human interleukin 17 receptor like protein, splice variant protein #10.
XX KW Human; receptor; Interleukin 17 receptor like protein; IL-17RL;
KW chondrocyte; bone degradation; cartilage degradation; gene therapy;
KW chromosome 3p25.3-3p24.1; rheumatoid arthritis; multiple sclerosis;
KW allergic skin immune response; organ transplant rejection; cytokine;
KW osteoarthritic; antirheumatic; antiarthritic; relapsing polychondritis;
KW seronegative spondyloarthritis; bone morphogenetic protein;
KW splice variant.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 612
XX FT /note= "Encoded by TC"
XX PN
XX PD WO200238764-A2.
XX PF 16-MAY-2002.
XX PR 13-NOV-2001; 2001WO-US43855.
XX PR 10-NOV-2000; 2000US-247134P.
XX PR 23-FEB-2001; 2001US-271197P.
XX PR 12-OCT-2001; 2001US-328904P.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Haudenschild D; Rose L, Moseley T, Reddi AH;
XX DR WPI; 2002-508211/54.
XX DR N-PSDB; ABK86557.
XX PT Interleukin-17 receptor-like polypeptide useful for the manufacture of
XX a medicament to modulate cartilage or bone growth in a mammal
XX Claim 1; Page 85-86; 108pp; English.
XX PS
XX XX

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CC The invention relates to an interleukin-17 receptor-like (IL-17RL)
CC polypeptide, with 85% or greater sequence identity to a polypeptide with
CC a sequence appearing as AAU98781-AAU98792, where IL-17RL binds
CC to an IL-17 selected from IL-17A, IL-17B, IL-17C, IL-17E and IL-17F.
CC Also included are IL-17RL polynucleotides, antibodies, expression
CC cassettes, transgenic host cells, a method of determining the
CC aggressiveness of a prostate cancer cell, by determining the presence or
CC absence in the cell of a group of IL-17RL (where the determination that
CC the group is absent in the cell indicates that the cancer is more
CC aggressive than a like cell in which the group is present) and a
CC mammalian cell comprising a polynucleotide encoding an IL-17B antagonist,
CC where the cell is selected from chondrocyte, synovioocyte, and mesenchymal
CC stem cell. IL-17RL or the polynucleotide is useful for the manufacture of
CC a medicament to modulate cartilage or bone growth in a mammal. The
CC polynucleotide is useful for the manufacture of a medicament to restore
CC androgen-responsiveness to a prostate cancer cell. IL-17RL is useful for
CC decreasing catabolic activity in bone or cartilage in a mammal. IL-17RL
CC is useful for inhibiting ossification or calcification in a mammal
CC suffering from pathological ossification or calcification, for diagnosing
CC a cartilage degenerative disorder in a mammal, for inhibiting the rate of
CC proteoglycan synthesis by a chondrocyte in culture, and for the
CC manufacture of a medicament to potentiate the activity of a bone
CC morphogenetic protein in a mammal. An IL-17RL antagonist is useful
CC for treating a bone or cartilage pathology such as a degenerative
CC cartilage disorder selected from osteoarthritis, rheumatoid arthritis,
CC relapsing polychondritis, seronegative spondyloarthropathies, multiple
CC sclerosis, allergic skin immune response and organ transplant rejection.
CC IL-17RL is particularly a receptor for IL-17B (Chondrocyte, a
CC proinflammatory cytokine). The gene for IL-17RL is located on
CC chromosome 3p25.3-3p24.1. The present sequence is the protein
CC sequence encoded by a splice variant of IL-17RL.
XX
SQ Sequence 703 AA;

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Query Match 96.0%; Score 3566.5; DB 23; Length 703;
Best Local Similarity 93.6%; Pred. No. 5e-317;
Matches 674; Conservative 1; Mismatches 0; Indels 45; Gaps 3;

QY 1 MPVPWFLSLALGRSPVLSRLERLVGPQDATHCSPGLSCRLWDSILCLPGDIVPAGPV 60
Db 1 MPVPWFLSLALGRSPVLSRLERLVGPQDATHCSPGLSCRLWDSILCLPGDIVPAGPV 60
QY 61 LAPTHLOTVLRLCQKETDCDCLLRVAVHLAVHGHWEPEDEKFGGAADSGVEEPRNAS 120
Db 61 LAPTHLOTVLRLCQKETDCDCLLRVAVHLAVHGHWEPEDEKFGGAADSGVEEPRNAS 120
QY 121 LOAQVVLSEFOAYPTARCVLLEVOVPAALYQFGSGSVYVDCFEAALGSSEVRITWSTQPR 180
Db 121 LOAQVVLSEFOAYPTARCVLLEVOVPAALYQFGSGSVYVDCFEAALGSSEVRITWSTQPR 180
QY 181 YEKELNHTQQLP-----ALPWLNVNSADGDNVHLVNLVNSEEQHFLSLYWN 225
Db 181 YEKELNHTQQLP-----ALPWLNVNSADGDNVHLVNLVNSEEQHFLSLYWN 240
QY 226 QVQGGPKPRWHKNTLGPQIITLNHTDLVPCLCIQVWPLEPDSVVRTNICFPREDPRAHQL 285
Db 241 QVQGGPKPRWHKNTLGPQIITLNHTDLVPCLCIQVWPLEPDSVVRTNICFPREDPRAHQL 300
QY 286 WQAAARLRLTLQSWLLDAPCSLPAEAAALCWAPGDPQCPPLVPLSWENVTVDKVFLEFPL 345
Db 301 WQAAARLRLTLQSWLLDAPCSLPAEAAALCWAPGDPQCPPLVPLSWENVTVDKVFLEFPL 353
QY 346 LKGGPNLVCQVNSSEKQLQECWLWADSLGPKDDVLLLETRGPQDNRSICALPSGCTSL 405
Db 354 -----VNSSEKQLQECWLWADSLGPKDDVLLLETRGPQDNRSICALPSGCTSL 403
QY 406 PSKASTRAARLGEYLQDLSGQCLQWDDDLGALWACPMKYIHKRWALVWLACLLFAA 465
Db 404 PSKASTRAARLGEYLQDLSGQCLQWDDDLGALWACPMKYIHKRWALVWLACLLFAA 463
QY 466 ALSLLILLKKDHAK-----AAARGRAALLYSDSGFERLVGALASALCOL 512
Db 464 ALSLLILLKKDHAKGWLRLKQDVRSAGAAAGRAALLYSDSGFERLVGALASALCOL 523

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PD 16-MAY-2002.

XX 13-NOV-2001: 2001WO-US43855.

XX 10-NOV-2000: 2000US-247134P.

PR 23-FEB-2001: 2001US-271197P.

PR 12-OCT-2001: 2001US-328904P.

XX (REG) UNIV CALIFORNIA.

PA Haudenschild D, Rose L, Moseley T, Reddi AH;

PI WPI: 2002-508211/34.

XX N-PSDB; ABR86556.

PT Interleukin-17 receptor-like polypeptide useful for the manufacture of
a medicament to modulate cartilage or bone growth in a mammal

PS Claim 1; Page 84; 108pp; English.

XX The invention relates to an interleukin-17 receptor-like (IL-17RL)
polypeptide, with 85% or greater sequence identity to a polypeptide with
a sequence appearing as AAU98781-AAU98792, where IL-17RL binds
to an IL-17 selected from IL-17A, IL-17B, IL-17C, IL-17E and IL-17F.
Also included are IL-17RL polynucleotides, antibodies, expression
cassettes, transgenic host cells, a method of determining the
aggressiveness of a prostate cancer cell, by determining the presence or
absence in the cell of a group of IL-17RL (where the determination that
the group is absent in the cell indicates that the cancer is more
aggressive than a like cell in which the group is present) and a
mammalian cell comprising a polynucleotide encoding an IL-17B antagonist,
where the cell is selected from chondrocyte, synovocyte, and mesenchymal
stem cell. IL-17RL or the polynucleotide is useful for the manufacture of
a medicament to modulate cartilage or bone growth in a mammal. The
polynucleotide is useful for the manufacture of a medicament to restore
androgen-responsiveness to a prostate cancer cell. IL-17RL is useful for
decreasing catabolic activity in bone or cartilage in a mammal. IL-17RL
is useful for inhibiting ossification or calcification in a mammal. IL-17RL
suffering from pathological ossification or calcification, for diagnosing
a cartilage degenerative disorder in a mammal, for inhibiting the rate of
proteoglycan synthesis by a chondrocyte in culture, and for the
manufacture of a medicament to potentiate the activity of a bone
morphogenetic protein in a mammal. An IL-17RL antagonist is useful
for treating a bone or cartilage pathology such as a degenerative
cartilage disorder selected from osteoarthritis, rheumatoid arthritis,
relapsing polycondritis, seronegative spondyloarthropathies, multiple
sclerosis, allergic skin immune response and organ transplant rejection.
IL-17RL is particularly a receptor for IL-17B (chondrocyte, a
proinflammatory cytokine). The gene for IL-17RL is located on
chromosome 3p25.3-3p24.1. The present sequence is the protein
sequence encoded by a splice variant of IL-17RL.

XX Sequence 693 AA;

Query Match 94.5%; Score 3510.5; DB 23; Length 693;
Best Local Similarity 92.2%; Pred. No. 6.7e-312;
Matches 664; Conservative 1; Mismatches 0; Indels 55; Gaps 3;

Qy 1 MPVPFLLSLALGRSPVLSRLVGVGPQDATHCSGLSRLWDSIILCLPGDIVPAPGV 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1 MPVPFLLSLALGRSPVLSRLVGVGPQDATHCSGLSRLWDSIILCLPGDIVPAPGV 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 LAPTHLQTLVLRCKETDCDCLRVAVHLAVHGWHEEPEDEKFGAADSGVEEPRNAS 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 LQAQVVLVFOAYPTARCVLLEQVPAALVQFGVSGSVVYDCFEAALGSEVRINWSTQPR 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 LQAQVVLVFOAYPTARCVLLEQVPAALVQFGVSGSVVYDCFEAALGSEVRINWSTQPR 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 181 YEKELNHTQQLP-----ALPWLNVSDAGDNVHLVNLVNSEQHFGLSLYWN 225
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 181 YEKELNHTQQLPDCRGLVWNSIPSCWALPWLNVSDAGDNVHLVNLVNSEQHFGLSLYWN 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 226 QVQGGPKPRWHKNTLGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHONL 285
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 241 QVQGGPKPRWHKNTLGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHONL 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 286 WQAARLRLTLTQSWLLDAPCSLPAEALCWRAFGGDPQCPPLVPPLSWENVTVDKVLFFPL 345
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 301 WQAARLRLTLTQSWLLDAPCSLPAEALCWRAFGGDPQCPPLVPPLSWENVTVDKVLFFPL 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 346 LKGHPNLCVOVNSSEKIQLOECLWADSLGPKDDVLLLETRGPDQNRSLCALPSSGCTSL 405
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 361 LKGHPNLCVOVNSSEKIQLOECLWADSLGPKDDVLLLETRGPDQNRSLCALPSSGCTSL 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 406 PSKASTRAARLGEYLLODLSQSGOCLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAA 465
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 421 PSKASTRAARLGEYLLODLSQSGOCLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAA 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 466 ALSLLILLKKDHAK-----AAARGRAALLLYSADDSGFERLVGALASALCQL 512
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 481 ALSLLILLKKDHAKGWLRLKQDVRSAGAAARGRAALLLYSADDSGFERLVGALASALC-- 538
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 513 PLRVAVDLMSRRRELSAQGPVAMFHAQRROTLOEGGVVLLFSPGAVALCSEWLQDGVSGP 572
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 539 -----QRROTLOEGGVVLLFSPGAVALCSEWLQDGVSGP 573
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 573 GAHGHDAFRASLSCLVLPDFLOGRAPGSYVGACFDRLHHPDAVPALFRTVPVTLFSQLP 632
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 574 GAHGHDAFRASLSCLVLPDFLOGRAPGSYVGACFDRLHHPDAVPALFRTVPVTLFSQLP 633
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 633 DFLGALQOPRAPRSRGRLOERAOVSRLQPALDSYFHPPTAPGRGVGPGAGGAGDGT 692
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 634 DFLGALQOPRAPRSRGRLOERAOVSRLQPALDSYFHPPTAPGRGVGPGAGGAGDGT 693
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Search completed: February 24, 2003, 09:22:33
Job time : 42 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 24, 2003, 09:21:11 ; Search time 18 Seconds
(without alignments)
1131.148 Million cell updates/sec

Title: US-09-608-918-2
Perfect score: 3716
Sequence: 1 MPVPWLLSLALGRSPVLS.....TPAPGRGVGPGAGCGDGT 692

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	326.5	8.8	617	4	US-09-188-930-303
2	174	4.7	866	2	US-08-620-694A-10
3	174	4.7	866	3	US-09-022-255-10
4	174	4.7	866	3	US-09-022-696-10
5	174	4.7	866	3	US-08-978-773-4
6	174	4.7	866	3	US-09-022-253-10
7	174	4.7	866	3	US-09-022-260-10
8	174	4.7	866	3	US-09-022-259-10
9	174	4.7	866	4	US-08-620-694A-2
10	165	4.4	864	2	US-09-022-257-10
11	165	4.4	864	3	US-09-022-255-2
12	165	4.4	864	3	US-09-022-696-2
13	165	4.4	864	3	US-08-978-773-2
14	165	4.4	864	3	US-09-022-253-2
15	165	4.4	864	3	US-09-022-260-2
16	165	4.4	864	4	US-09-022-259-2
17	165	4.4	864	4	US-09-022-257-2
18	162	4.4	330	4	US-09-188-930-125
19	116.5	3.1	1711	2	US-08-342-930-2
20	112.5	3.0	1208	4	US-09-463-702A-2
21	108	2.9	2629	2	US-08-751-189-4
22	108	2.9	2629	2	US-09-060-836-4
23	108	2.9	2629	4	US-09-184-445-4
24	107	2.9	4928	4	US-09-036-987A-5
25	107	2.9	4928	4	US-09-370-700-5
26	106	2.9	449	3	US-08-897-236-23
27	103.5	2.8	3739	3	US-09-320-878-2

28	101.5	2.7	469	3	US-08-753-007A-8	Sequence 8, Appli
29	101.5	2.7	469	4	US-09-398-496-8	Sequence 8, Appli
30	100	2.7	954	2	US-08-749-169A-3	Sequence 3, Appli
31	100	2.7	954	2	US-09-130-032A-3	Sequence 3, Appli
32	99	2.7	3724	2	US-08-804-227C-10	Sequence 10, Appl
33	99	2.7	3724	2	US-08-804-198-4	Sequence 4, Appli
34	98	2.6	623	1	US-08-653-740-7	Sequence 7, Appli
35	98	2.6	623	2	US-09-073-594-7	Sequence 7, Appli
36	98	2.6	623	3	US-09-275-925-7	Sequence 7, Appli
37	98	2.6	2205	1	US-08-093-453B-2	Sequence 2, Appli
38	97.5	2.6	647	3	US-08-753-007A-32	Sequence 32, Appl
39	97.5	2.6	647	4	US-09-398-496-32	Sequence 33, Appl
40	97.5	2.6	3739	4	US-09-105-537-33	Sequence 6, Appli
41	97.5	2.6	11877	4	US-09-105-537-6	Sequence 5, Appli
42	97	2.6	1326	4	US-09-147-236-5	Sequence 4, Appli
43	96.5	2.6	579	4	US-09-171-710-6	Sequence 50, Appl
44	96	2.6	405	2	US-08-483-151-4	
45	96	2.6	1843	4	US-09-413-814-50	

ALIGNMENTS

RESULT 1
US-09-188-930-303
; Sequence 303, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Orust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-303

Query Match	8.8%	Score 326.5	DB 4	Length 617
Best Local Similarity	26.7%	Pred. NO. 1.4e-22		
Matches 132	Conservative 56	Mismatches 184	Indels 123	Gaps 19
Qy	237	KNLTGPQIITLNHTDLVPCLCIQVNPDPDPSVTRNTICPFREDPRAH-QNLWQAR----	290	
Db	183	KIVSGGHTVDLPEYFLPCMCIEASYLOEDTVRRKCPQSWPEAYGDFWQSIRTDYS	242	
Qy	291	-----LRLLTQSLLWLDAPCSLPAAALCWRAPGGDPCQPLVPLPSWENVTVDKVLEFPL	345	
Db	243	QHNOVMVMTLR-----CPLKLEASLCWRQDPLTPCETL-----PNATAQESGWI	289	
Qy	346	LKG---HNPCLQVNSSEKLOEQELWADSLGPLKDDVLLLETRGPQDNRSLCALEPSCG	402	
Db	290	LENVDLHPQLCFKF-SFENSSHVEC--PHQSGSLPSWTVMSTQAOQ-----LTLHFSSR	341	
Qy	403	TSLPSKASTRAARLG-----EVLLODLOGGCLQIWDLDDLGAL	440	
Db	342	TYATFSAWSDFGLGPDTPMPVPVVISOTQGSVPVTVTLTIIPFLROENCILVMRSDVHFA	401	
Qy	441	W---ACPMKDYIHKRWALVWLACLFLFAAALSLLLLKDKHAKAARGAALLYSADDSG	497	
Db	402	WKHVLCPDD-----APYPTQLLR-----SLGSGTRPVLLLHHAADSEA	440	
Qy	498	FERLVGALASALCOLPURA-----VDLWSRRELSAQGPVAFHQRQTLOEGGVV	549	
Db	441	QRRVLGALAEI-----LRTALGGGRDVIVDLWEGTHVARIGPLPLWLAARVAREQGTV	495	

Query Match 4.7%; Score 174; DB 3; Length 866;
Best Local Similarity 21.6%; Pred. No. 1.1e-07;
Matches 119; Conservative 76; Mismatches 189. Indels 1

```
QY 237 KNL--GPOIITLN-----HT---DLVPCLCIQVWPLEPDS-----VRTN--- 271
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 66 RNLTPSPKDLQIQHFAHTQOGLFPVAHIE-WTLQTDASILYLEGAELSVLQLTNR 124
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 272 IC---PFREDPRAHQLWQAARLRLTLQSWLLDAPCS-----LPAEALCWAPGPD 321
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 125 LCVRFEEFLSKLRHHRWR-----FTSFHVDPDQYEVYVTHLPKP-----IPDGD 172
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 322 PCOP-----LVPPLSWENVTVDKVLEPFLKLG-----HPNLCVQVNSSEKLOQLQCLWADSL 373
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 173 PNHQSKNFLVPDCEHARMKVT-----PCMSSGSLWDPNITVETLEAHQLRVSTLWNES- 227
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 374 GPLKDDVLLLETGPDNRSLCALEPSGCTS-----LPSKASTRAARLGEY-----LL 421
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 228 ---THYQIILLTSFPH-----MENHSCFEHMHIP-----APRPEEFHQRSNVTTLT 270
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 422 QDLQS-----GOCQLQWDDDL--GALWACP-----MDKYIHKRWAL 455
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 271 RNLKGCRRHQVQIOFPFSSCL-----NDCLRHSATVSCPEMPDTPPIPDYMLWVY--WFI 325
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 456 VMLACLLFAAALSLLILK-----KDHAKEA-----ARGRAALLYS 492
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 326 TGISILLVGSVILLIVCMTWRLAGPGESEKYSDDTKYTDGLPAADLIPPLPKRWIIYS 385
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 493 ADDSGFERLVGALAS-ALCOLPLRVAVDLWSRRELSAQGPVAMFHAQRRTQLQEGGVVYL 551
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 386 ADHPLYVDVWLKFAQFLLTACGTEVALDLEEQAISEAGVMTWVGROKQEMVESNSKIIV 445
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 552 LPSGVALCSEWLQDGVSGPA-----HGP--HDAFRASLSCVLPDFLQGRAPGSYV 602
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 446 LCSRGTRA---KW--QALLGRGAPVRLRCDHGRKPVGDLFTAAMNMILPDFKRPACFGTYV 500
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 603 GACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLQALQOPRAPRSGRLOQRAEOYSRALQP 662
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 501 VCYFSEVSCDGDVDFLFGAAPRYPLMDRFEVYFRIDLEMFQPGRM-HRVGELSG----- 555
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 663 ALDSYFHPGP 672
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 556 --DNVLRSPG 563
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
```

RESULT 7

```
US-09-022-260-10
: Sequence 10, Application US/09022260
: Patent No. 6100235
: GENERAL INFORMATION:
: APPLICANT: Yao, Zhengbin
: APPLICANT: Spriggs, Melanie
: APPLICANT: Fanslow, William
: TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: City: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Apple, Version 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/022,260
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/620,694
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-260-10

Query Match 4.7%; Score 174; DB 3; Length 866;
Best Local Similarity 21.6%; Pred. No. 1.1e-07;
Matches 119; Conservative 76; Mismatches 189; Indels 166; Gaps 32;

QY 237 KNL--GPOIITLN-----HT---DLVPCLCIQVWPLEPDS-----VRTN--- 271
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 66 RNLTPSPKDLQIQHFAHTQOGLFPVAHIE-WTLQTDASILYLEGAELSVLQLTNR 124
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 272 IC---PFREDPRAHQLWQAARLRLTLQSWLLDAPCS-----LPAEALCWAPGPD 321
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 125 LCVRFEEFLSKLRHHRWR-----FTSFHVDPDQYEVYVTHLPKP-----IPDGD 172
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 322 PCOP-----LVPPLSWENVTVDKVLEPFLKLG-----HPNLCVQVNSSEKLOQLQCLWADSL 373
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 173 PNHQSKNFLVPDCEHARMKVT-----PCMSSGSLWDPNITVETLEAHQLRVSTLWNES- 227
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 374 GPLKDDVLLLETGPDNRSLCALEPSGCTS-----LPSKASTRAARLGEY-----LL 421
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 228 ---THYQIILLTSFPH-----MENHSCFEHMHIP-----APRPEEFHQRSNVTTLT 270
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 422 QDLQS-----GOCQLQWDDDL--GALWACP-----MDKYIHKRWAL 455
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 271 RNLKGCRRHQVQIOFPFSSCL-----NDCLRHSATVSCPEMPDTPPIPDYMLWVY--WFI 325
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 456 VMLACLLFAAALSLLILK-----KDHAKEA-----ARGRAALLYS 492
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 326 TGISILLVGSVILLIVCMTWRLAGPGESEKYSDDTKYTDGLPAADLIPPLPKRWIIYS 385
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 493 ADDSGFERLVGALAS-ALCOLPLRVAVDLWSRRELSAQGPVAMFHAQRRTQLQEGGVVYL 551
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 386 ADHPLYVDVWLKFAQFLLTACGTEVALDLEEQAISEAGVMTWVGROKQEMVESNSKIIV 445
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 552 LPSGVALCSEWLQDGVSGPA-----HGP--HDAFRASLSCVLPDFLQGRAPGSYV 602
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 446 LCSRGTRA---KW--QALLGRGAPVRLRCDHGRKPVGDLFTAAMNMILPDFKRPACFGTYV 500
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 603 GACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLQALQOPRAPRSGRLOQRAEOYSRALQP 662
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 501 VCYFSEVSCDGDVDFLFGAAPRYPLMDRFEVYFRIDLEMFQPGRM-HRVGELSG----- 555
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 663 ALDSYFHPGP 672
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 556 --DNVLRSPG 563
:|||||: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||

RESULT 8
US-09-022-259-10
: Sequence 10, Application US/09022259
: Patent No. 6191104
: GENERAL INFORMATION:
: APPLICANT: Yao, Zhengbin
: APPLICANT: Spriggs, Melanie
: APPLICANT: Fanslow, William
: TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
: NUMBER OF SEQUENCES: 10
```


CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
...
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,259
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-259-10

	Query Match	4.78;	Score 174;	DB 4;	Length 866;	32;
	Best Local Similarity	21.6%;	Pred. No. 1.1e-07;			
	Matches 119; Conservative	76;	Mismatches 189;	Indels 166;	Gaps	
QY	237 KNLT--GPOIITLN-----HT---DLVCLCCTQVWPLEPDS-----VRTN--	--	271			
	: : : : : :	:	:	:	:	:
Db	66 RNLTPSPKDIQLQHFAHQOGLDFPVAHIE-WLQTDA SILYLEGAELSVLOLNTNER	124				
QY	272 IC---PEREDPRAHQNLUQAARLLRLTLQSLLDAPCS-----LPAAALCWRAPCGD	321				
	: : : : : :	:	:	:	:	:
Db	125 LCVRFELSRLRHRRWR-----FTFSHEVDPDQEYEVTVIHLKP-----IPDG	172				
QY	322 PCQP---LYPPISWENVTVDKVLFFLLKG-----HPNLVCQVNSSSEKLQOECLWADSL	373				
	: : : : : :	:	:	:	:	:
Db	173 PNHQSKNFLVPDCGEHARMKVTT-----PCMSSGLWDPNITVETLEAHLRVSF-TLWNES-	227				
QY	374 GPLKDVVLLLETGPQDNRSICALPESGCTS----LPSKASTRAARGEY-----LL	421				
	: : : : : :	:	:	:	:	:
Db	228 ----THYQILLTSFPH-----MENISCHEMHMHIIP-----APRPEEFHORSNVLTLT	270				
QY	422 QDLQS-----GCQLWDDDL--GALWACP-----MDKYTHKKRWAL	455				
	: : : : : :	:	:	:	:	:
Db	271 RNLKGGCRHHQVQIQPFSSCL----NDCLRHSATWSCPEMPDTPEPIPYDMPLWYY--WFI	325				
QY	456 VWLAACLILFAALSILILIK-----KDHAKEA-----ARGRAALLLYS	492				
	: : : : : :	:	:	:	:	:
Db	326 TGISILLGVSVILLIVCMTWRLAGPGSEKYSDDTKYTDDLPAADLIPLPKRKRWIIYS	385				
QY	493 ADDSGFERLVGALAS-ALCOLPLRVAVLDWSRRRELSAQGPVAWFHAORROTLOBGGVVWL	551				
	: : : : ~~~~~~:	:	:	:	:	:
Db	386 ADHPLYVDVVKLFKAQFLLTAGCTEVALDLLLEQAIISBAGYMTWGROKQEMVSNSKIIV	445				
QY	552 LHSPGAVALCSEWLQDVSGPGA-----HGP--HDFAFRASILSCVLPFLQGRAPGSYV	602				
	: : : : : :	:	:	:	:	:

```

Db      446  LCSRGT---KW--QALLRGAPVRLRCDHGKPVGDLFTAAANNMILPDFKRPACFGTYV 500
Qy      603  GACDRLLHDPADVPALFRTVPVFTLPSQLDFLGAQQPAPSGRLQERAEQVSRALQP 662
Db      501  VCIFYEVSCDGDPDLFGAAPRPLMDRFEVYFRIQDLEMFQGRM-HRVGELSG-----555
Qy      663  ALDSYFHPGP 672
Db      556  --DNYLRSPG 563

RESULT 9
US-09-022-257-10
; Sequence 10, Application US/09022257
; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257

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[illegible]

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Db 173 PNHGSKNPLFVPCDEHAKMKT-----PCMSGSLMDNITVETLEAHQLRVSTLWMS- 227
Oy 374 GPLKDDVLLFTRGRPODNRSLALEPSGCTS---LPSKASTRAARLGEY-----LL 421
Db 228 ----THYQILITSEPH-----MENNSCFEHMHHP-----APREPEFORSVTLTL 270
Oy 422 QDLQS-----GCCQLQMDL--GALMACP-----MDKYIHKRWAL 455
Db 271 RNLKGGCRHVOVQIOPFSSCL---NDCLRHSATVSCPEMDTPRPIDYMLWY--WFI 325
Oy 456 VMLACLFAALSLILLK-----KDHAKA-----AGRAALLYS 492
Db 326 TGISILVGSVILLVCMWRLAGPSEKYSDDTKYTDGLPAADLPPPLKPRVWIIYS 385
Oy 493 ADDSGEERLVGALAS--ALCOLPLRVAVDLMSRRELNAOGVAVMFHAROTLOSGVVL 551
Db 386 ADHPLVDVVLKFAOFLITACGTEVALDLLEQAISEAGVMTWYGRKQOEAVESNKITV 445
Oy 552 LPSGAVALCSEMLQDVGSGPGA-----HGP--HDAFRASLSCVLPDLQGRAPGSYV 602
Db 446 LCSRGRFA--KW--QALLGRGAPVRLRCDHGKPVGDLFTAAAMNMLLPDFRRACFGTYV 500
Oy 603 GACFDRLLHPDAVPALFRVYVFTLPSQLPDLGALQDPRAPNSGRLOERAOVSRLQOP 662
Db 501 VCYFSEVSCDGDVVDLFGAAPRYPLMDREEVYFRIDLEMFQGRM--HRVGEISG---- 555
Oy 663 ALDSYFHPG 672
Db 556 --DNYLRSPG 563

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RESULT 10

US-08-620-694A-2

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; Sequence 2, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Power Macintosh
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206)

```

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-620-694A-2

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Query Match 4.4%; Score 165; DB 2; Length 864;
Best Local Similarity 19.8%; Pred. No. 7,7e-07;
Matches 123; Conservative 79; Mismatches 209; Indels 210; Gaps 31;

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Oy 192 PALPW-----LANSADGDNVLYLN-----VSEEDHFGSLTYMNOVGPP--KPRM--HKML 239
Db 14 PALGMLLLLVNLAIPGRASPRLLDPAPYCAOE--GLSC--RVKSTCLDSMHPKML 68
Oy 240 T--GFOITLN-----HTDLVPLCICVWPLEPDS-----VFTN--IC- 273
Db 69 TPSSPKNIYINLSVSTQGEIVPLVHVE--WLOTDAISILEGAEISVLQNTNRLCY 127
Oy 274 --PREDPRAHONLQOARLRLTLQSLMDAPCSLPAAE-----ALCMRAPGDP--- 322
Db 128 KFQFLSMLOHHRKRMF-----FESHFVVD-----PGQEEYEVYVHNLPRKPIPDGDPNHR 176
Oy 323 -----CQPLVPLSMENVTYDKVLEPRLKGNPLCVQVNSRKLQDECTMADSLG 374
Db 177 SKLIIVPDCEDSKMKMTTSVSSGSLMD-----PNITVEITDQLRLDFTLMNEST- 228
Oy 375 PLKDDVLLFTRGRPODNRSLALEPSGCTS-----PSKASTRAARLGEYLLQDLSQ 428
Db 229 PYQ--VLESFSDSEHNS-----CFDVYKQIFARPQDEHNOANVTFLSKFH--- 274
Oy 429 CLQMDDDLGLMAC-----PMDKYIHR 452
Db 275 -----WCCHHNVQVOPFSSCLNDCLRHAVTVPCEVISNTGYPKPVADYI--PL 321
Oy 453 WA--LWMLACLFAALSLILLK-----KDHAKAARGA 486
Db 322 WYGLITLAILLVGSVYLLICMTWRLSGADQEKHGDSKINGILPVADLPPPLRPRK 381
Oy 487 ALLIYSADSGFERLVGALASAL--COLPLRVAVDLMSRRELNAOGVAVMFHAROTLO 545
Db 382 VWIYVSADHPLVEVYLKFAOFLITACGTEVALDLLEQVISEAGVMTWYGRKQOEAVS 441
Oy 546 GGVVLLFSPG-----AVAL--CSEMLQDVGSGPGAHPDAFRASLSCVLP 590
Db 442 NSKIIILCSRGTOAKKKAIIIGWAEPAYOLRCDHMKPAG-----DLFTAAAMNMLP 491
Oy 591 DFLQGRAGSYGACFDRLHPDAVPALFRVYVFTLPSQLPDLGALQDPRAPNSGRLO 650
Db 492 DFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPLMDREEVYFRIDLEMFEGRMH 551
Oy 651 ERAOVSRALQPALDSYFHP 671
Db 552 HVRELTG-----DNYLQSP 565

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RESULT 11

US-09-022-255-2

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; Sequence 2, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA

```

ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/620,694

FILING DATE: 21 MARCH 1996

APPLICATION NUMBER: USSN 08/538,765

FILING DATE: 7 AUGUST 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 864 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-022-255-2

Query Match 4.4%; Score 165; DB 3; Length 864;
Best Local Similarity 19.8%; Pred. No. 7.7e-07;
Matches 123; Conservative 79; Mismatches 209; Indels 210; Gaps 31;

QY 192 PALPW---LNVADGDNVHLVNLN---VSEHQHGLSLYWNQVQGP--KPRW--HKNL 239
DB 14 PALGWLILLNVLAPGRASPRLLDFPAPVCAQE--GLSC---RVKNSTCLDSDWIHPKNL 68
QY 240 T--GPQIITLN-----HTDLVPCLCIQVWPLEPDS-----VRTN--IC- 273
DB 69 TPSSPKNIYINLSVSTQHGELVPVLHVE-WTLDQDASLYLEGAELSVLQLTNERLCV 127
QY 274 --PFREDPRAHONLWOARLLTLTQSWLLDAPCSLPABA-----ALCWAPGGDP-- 322
DB 128 KFQFLSMLOHHRKWR-----FSESHFVVD-----PGQEVETVHHLPKPIPDGDPNHK 176
QY 323 -----CQPLVPPLSWENVTVDKVLEFPLKLGHPNLCVQVNSSEKLOLQECLEWADSLG 374
DB 177 SKIIFVPDCDSKMKMTTSCVSSGSLWD-----PNITVETLDQHLKRVDFTLWNEST- 228
QY 375 PLKDDVILLETGRPDNRSLCALEP SGCTSL-----PSKASTRAARLCEYLLODLQSGQ 428
DB 229 PYQ---VLLESFSDSENHS-----CFDVVKQIFAPRQEEFORANVTFLSKFH--- 274
QY 429 CLQWDDDLGLWAC-----PMDKIYIHR 452
DB 275 -----WCCHHHVQVQPFSSCLNCLRHAVTPCPVISNTTVPKPVADYI-PL 321
QY 453 WA---LVWLACLLFAAALSLILLK-----KDHAKAAGRA 486
DB 322 WVYGLTLIAILLVGSIVILITCMTRWLSGADQEKHGDDSKINGILPVADLTTPPLRPK 381
QY 487 ALLYSADDSGFERLVGALASAL-CQLPLRVAVDLWSRRELSAQCQPVAFHQRQTLOE 545
DB 382 WVIYSADHPLLYEVVLKFAQLITACGTEVALDLEEQVISEVGVMTVWSRQKQEVES 441
QY 546 GGVVLLFSPG-----AVAL-CSEWLQDGVSGPGAGHPHDAFASLSCVLP 590
DB 442 NSKIIILCSRGTOAKMKAILGWAEPVQLRCDHKNKPG-----DLFTAAANNMILP 491

QY 591 DFLQGRAPGSYVACDFDRLLHPDAVPALFRTYVFTLPQLDFLGNALQOPRAPRSRLQ 650
DB 492 DFKRACFTGYVVCYFSGICSERDVPDLFNITSRYPLMDRFEVYFRIODLEMFEPGRMH 551
QY 651 ERAEQVSRLQPALDSYFHP 671
DB 552 HVRELTG-----DNYLQSP 565

RESULT 12

US-09-022-696-2

Sequence 2, Application US/09022696

Patent No. 6072037

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,696

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/620,694

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 864 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-022-696-2

Query Match

4.4%; Score 165; DB 3; Length 864;

Best Local Similarity 19.8%; Pred. No. 7.7e-07;

Matches 123; Conservative 79; Mismatches 209; Indels 210; Gaps 31;

QY 192 PALPW---LNVADGDNVHLVNLN---VSEHQHGLSLYWNQVQGP--KPRW--HKNL 239
DB 14 PALGWLILLNVLAPGRASPRLLDFPAPVCAQE--GLSC---RVKNSTCLDSDWIHPKNL 68
QY 240 T--GPQIITLN-----HTDLVPCLCIQVWPLEPDS-----VRTN--IC- 273
DB 69 TPSSPKNIYINLSVSTQHGELVPVLHVE-WTLDQDASLYLEGAELSVLQLTNERLCV 127
QY 274 --PFREDPRAHONLWOARLLTLTQSWLLDAPCSLPABA-----ALCWAPGGDP-- 322
DB 128 KFQFLSMLOHHRKWR-----FSESHFVVD-----PGQEVETVHHLPKPIPDGDPNHK 176

Qy	323	-----CQPLVPPLSWENVTDKVLFEFLLKHPNLCVQVNSSEKLOLOECLWADSLG	374
Db	177	SKLIIFVPDCEDSKMKMTSCVSSGLWD-----PNITVETLDTQHLRVDFTLWNEST-	228
Qy	375	PLKDDVLLLETRGPDNRNSCALEPSCCTSL-----PSKASTRAARLGEYLLQDLOSGO	428
Db	229	PYQ---VLLSEFSDSENHS-----CFDVVKQIFAPROEEFHQANVTFTLSKFH-----	274
Qy	429	CLQLWDDDLGALWAC-----PMDKVIHKR	452
Db	275	-----WCCHHVQVQPFSSCLNDCLRHAHVTPCPVISNTVPKPVADVII-PL	321
Qy	453	WA-----LVWLACLLFAAALSILLLK-----RDHAKAARGRA	486
Db	322	WVYGLITLAIILVGSVIVILICMTWRLSGADQEKHGDDSKINGILPVADLTPTPLPRPK	381
Qy	487	ALLYSADDSCEFERLVGALASAL-CQLPLRVAVDILMSRRSELSAQGPVAFHQAQRROTLOE	545
Db	382	WVIYVSADHPLYVEVVLKFAQFLITACGTGEVALDLEBQVISEGVYMTWWSROKQEMVES	441
Qy	546	GGVVVLLFSPG-----AVAL-CSEWLQDGVSGGCAHPHDAFRASLCVLP	590
Db	442	NSKIIILCSRGTOAKMKAILGWAEPAVOLRCDHWKPAQ-----DLFTAAMNMLP	491
Qy	591	DFLQGRAPGSVYGACFDRLHHPDAVALPRTVPVFTLPSQLPDFLGCALQOPRAPSRLQO	650
Db	492	DFKRPACFGYVVCYFSGICSEKRDVDDNITSRYPLMDRFEVEVYFRIODLEMFEPGRMH	551
Qy	651	ERAEQVSRALQPADLSYFHPP	671
Db	552	HVRELTG-----DNYLOSP	565

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1  RESULT 13
2  US-08-978-773-2
3  ; Sequence 2, Application US/08978773
4  ; Patent No. 6083906
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Troutt, Anthony
7  ; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
8  ; NUMBER OF SEQUENCES: 4
9  ; CORRESPONDENCE ADDRESS:
10 ; ADDRESSEE: Immunex Corporation
11 ; STREET: 51 University Street
12 ; CITY: Seattle
13 ; STATE: WA
14 ; COUNTRY: USA
15 ; ZIP: 98101
16 ; COMPUTER READABLE FORM:
17 ; MEDIUM TYPE: Floppy disk
18 ; COMPUTER: Apple PowerMacintosh
19 ; OPERATING SYSTEM: Apple Operating System 7.5.5
20 ; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
21 ; CURRENT APPLICATION DATA:
22 ; APPLICATION NUMBER: US/08/978,773
23 ; FILING DATE:
24 ; CLASSIFICATION: 530
25 ; PRIOR APPLICATION DATA:
26 ; APPLICATION NUMBER: USSN 60/052,525
27 ; FILING DATE: 27 NOVEMBER 1996
28 ; CLASSIFICATION: 530
29 ; ATTORNEY/AGENT INFORMATION:
30 ; NAME: Perkins, Patricia Anne
31 ; REGISTRATION NUMBER: 34,693
32 ; REFERENCE/DOCKET NUMBER: 2623-A
33 ; TELECOMMUNICATION INFORMATION:
34 ; TELEPHONE: (206)587-0430
35 ; TELEFAX: (206)
36 ; INFORMATION FOR SEQ ID NO: 2:
37 ; SEQUENCE CHARACTERISTICS:
38 ; LENGTH: 864 amino acids
39 ; TYPE: amino acid

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;          TOPOLOGY: linear
;          MOLECULE TYPE: protein
US-08-978-773-2

Query Match          4.4%; Score 165; DB 3; Length 864;
Best Local Similarity 19.8%; Pred. No. 7.7e-07;
Matches 123; Conservative 79; Mismatches 209; Indels 210; Gaps

QY 192 PALPW-----LNVSADGDNVHLVN-----VSEQHFGLSLYNOVGQPP--KPRW--HKNL 239
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 14 PALGWLIIILNVLAPGRASPRLLDPFAPVCAQE--GLSC--RVKNSCTLDDSWIHKPL 68

QY 240 T--GQIITLN-----HTDLVPCLCITQVWPLEPDS-----VRTN--IC- 273
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 69 TPSSPKNYIINLSVSSQTGELVPVLHVE--WTLOTDAILYLEGAELSVLQLTNERLCV 127

QY 274 --PPREDPRAHONLWQAARLLTLTQSLWLLDAPCSLPAE-----ALCWRAFGDP-- 322
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 128 KFQFLSMLOHHRKWR-----FSFSEHVD-----PGQEYEVTVHHLPRKIPDGDPNHK 176

QY 323 -----CQPLVPPLSWENYTVDKVLEFFLLKGHPNLCVGVNSSEKILQLOECILWADSLG 374
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 177 SKIIFVPDCEDSKMKWTTCVSSGSLWD-----PNITVETLDTQHLRVDFTLWNEST- 228

QY 375 PLKDDVILLETFRGQDNRSLCALFPGSGCTSL-----PSKASTRAARLGEYLLQDLSGQ 428
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 229 PYQ--VVLESFDSSENHS-----CFDVVKQIFAPRQEEPHQRAENVITFLTSKPH-- 274

QY 429 CLQLWDDDLGALWAC-----PMDKYIHKR 452
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 275 -----WCCHHHVQVQPFSSCLNDCLRHAVTVFCPVISNTVTKPVADYIT-PL 321

QY 453 WA---LYWLACLLEFAAALSLLILK-----KDHAKAAAGRA 486
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 322 WYGLITLIAIIIVGSVTVLIICITWRLSGADQEKHGDDSKINCILPVADITPPPLPRK 381

QY 487 ALLIYSADDSGFERLVGALASAL--COLPLRVAVDLMSRRLESAQGPVAFHQRRTLQE 545
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 382 VWIYVSADHPLYVEWVLKFAQGLITACGTGTEVALDLEEQVISEVGVMTWYSRQKQEMVES 441

QY 546 GGVVVLLFSPG-----AVAL--CSEHWLDQVSGPGAHGPHDAFRASLSCLVP 590
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 442 NSKIIILCSRGTOAKKAILGWAEPAVOLRCDHKKPAG-----DLFETAMNMLP 491

QY 591 DFLQGRACPSYVGACFDRLHLHPDAVPALEFVTVFTLPSPOLPDFLGAQPPAPRSRGLQ 650
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 492 DFKRPACFGTVVVCYFSGICSERDVPDLFNITSRYPLMDRFEVYFRIQDLEMFEPFGR 441

QY 651 ERAEQVSRALQPADLSYFHPP 671
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 552 HVRELTG-----DNYLOSP 565
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,773
FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/052,525

FILING DATE: 27 NOVEMBER 1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 24 002

REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2622-2

REFERENCE/DOC#1 NUMBER: 2023-A
TELECOMMUNICATION INFORMATION.

TELEPHONE: (206) 587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 864 amino acids

TYPE: amino acid


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Db 177 SKIIFVPCEDSKMKWTSCVSSGSLWD-----PNITVETLDTQHLRVDFTLWNEST- 228
QY 375 PLKDDVLLLETRGPDNRSLCALEPFGCTSL-----PSKASTRAARLGEYLLQDLQSGQ 428
Db 229 PYQ---VLLESFSDSENHS-----CFDVVVKQIFAPROEEFHORANVTFTLSKPH--- 274
QY 429 CLQLWDDDLGALWAC-----PMDKYIHKR 452
Db 275 -----WCCHHHVQVQPFSSCLNDCLRHAVTVPCPVISNTTVPKPVADYI-PL 321
QY 453 WA---LVWLACLLFAAALSLLLEK-----KDHAKAAARGRA 486
Db 322 WYGLTLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKINGILPVADLTTPPLRPK 381
QY 487 ALLYSADDSGFERLVGALASAL-CQLPLRVAVDLWSRRELSAOGPVAVFWFAORRQTLQE 545
Db 382 VWIVYSADHPLYVEVLKFAOFLITACGTEVALDLLEEQVISEVGVMTWVSQKQEMVES 441
QY 546 GGVVLLFSPG-----AVAL-CSEWLQDGVSGFGAHGPHDAFRASLSCVLP 590
Db 442 NSKIIILCSRGTOAKWKAILGWAEPVQLRCDHWKPG-----DLTTAAMMILP 491
QY 591 DFLQGRAPGSYVGACFDRLHPDAVPALFRTVPVETLPSQLPDFLGALQQPRAPRSRLQ 650
Db 492 DFRPACFGTYVVCYFSGICSERDVPDLNITSRYPLMDRFEVYFRIQDLEMFEPRMH 551
QY 651 ERAEQVSRALQPALDSYFHP 671
Db 552 HVRELTG-----DNYLOSP 565

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Search completed: February 24, 2003, 09:23:54
Job time : 24 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 24, 2003, 09:22:01 ; Search time 14 Seconds
(without alignments)
1535.737 Million cell updates/sec

Title: US-09-608-918-2
Perfect score: 3716
Sequence: 1 MPVPFWLLSLALGRSPVLS.....TPAPGRGVGPGAGPCAGDGT 692

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3716	100.0	692	10	US-09-899-471-8 - 2003
2	3699.5	99.6	705	9	US-09-874-503-14 - 2003
3	3699.5	99.6	705	9	US-10-000-157-14
4	3699.5	99.6	705	9	US-10-063-547-162
5	3699.5	99.6	705	9	US-09-816-744-14
6	3699.5	99.6	705	9	US-09-747-259-14
7	3699.5	99.6	705	9	US-10-174-590-598
8	3699.5	99.6	705	9	US-10-176-758-598
9	3699.5	99.6	705	9	US-10-063-616-162
10	3699.5	99.6	705	9	US-10-175-737-598
11	3699.5	99.6	705	9	US-10-063-502-162
12	3699.5	99.6	705	9	US-10-173-706-598
13	3699.5	99.6	705	9	US-10-175-738-598
14	3699.5	99.6	705	9	US-10-175-752-598
15	3699.5	99.6	705	9	US-10-176-482-598
16	3699.5	99.6	705	9	US-10-176-757-598
17	3699.5	99.6	705	9	US-10-176-913-598
18	3699.5	99.6	705	9	US-10-180-552-598
19	3699.5	99.6	705	9	US-10-180-557-598

20	3699.5	99.6	705	9	US-10-173-700-598	Sequence 598, App
21	3699.5	99.6	705	9	US-10-174-572-598	Sequence 598, App
22	3699.5	99.6	705	9	US-10-174-579-598	Sequence 598, App
23	3699.5	99.6	705	9	US-10-174-582-598	Sequence 598, App
24	3699.5	99.6	705	9	US-10-175-588-598	Sequence 598, App
25	3699.5	99.6	705	9	US-10-175-739-598	Sequence 598, App
26	3699.5	99.6	705	9	US-10-175-740-598	Sequence 598, App
27	3699.5	99.6	705	9	US-10-175-743-598	Sequence 598, App
28	3699.5	99.6	705	9	US-10-176-488-598	Sequence 598, App
29	3699.5	99.6	705	9	US-10-176-492-598	Sequence 598, App
30	3699.5	99.6	705	9	US-10-176-747-598	Sequence 598, App
31	3699.5	99.6	705	9	US-10-176-750-598	Sequence 598, App
32	3699.5	99.6	705	9	US-10-176-985-598	Sequence 598, App
33	3699.5	99.6	705	9	US-10-176-987-598	Sequence 598, App
34	3699.5	99.6	705	9	US-10-176-991-598	Sequence 598, App
35	3699.5	99.6	705	9	US-10-176-992-598	Sequence 598, App
36	3699.5	99.6	705	9	US-10-176-993-598	Sequence 598, App
37	3699.5	99.6	705	9	US-10-184-658-598	Sequence 598, App
38	3699.5	99.6	705	9	US-10-173-695-598	Sequence 598, App
39	3699.5	99.6	705	9	US-10-173-697-598	Sequence 598, App
40	3699.5	99.6	705	9	US-10-173-705-598	Sequence 598, App
41	3699.5	99.6	705	9	US-10-174-576-598	Sequence 598, App
42	3699.5	99.6	705	9	US-10-174-585-598	Sequence 598, App
43	3699.5	99.6	705	9	US-10-174-586-598	Sequence 598, App
44	3699.5	99.6	705	9	US-10-175-747-598	Sequence 598, App
45	3699.5	99.6	705	9	US-10-176-481-598	Sequence 598, App

ALIGNMENTS

RESULT 1

US-09-899-471-8
; Sequence 8, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 8
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Human
US-09-899-471-8

Query Match 100.0%; Score 3716; DB 10; Length 692;
Best Local Similarity 100.0%; Pred. No. 1.7e-296;
Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MPVPFWLLSLALGRSPVLSLRLVGPQDATHCSPGLSCRLWDSILCLPGDIVPAPGV	60
Qy	61	LAPTHLQTELVLRCOKETDCDLCLRVAVHLAVGHWEPEDEKFCGAADSGVEEPNNA	120
Db	61	LAPTHLQTELVLRCOKETDCDLCLRVAVHLAVGHWEPEDEKFCGAADSGVEEPNNA	120
Qy	121	LQAOVLSFQAYPTARCVLLEVQVPAALVQFGOSGVSVYDCFEAALGSEVRWSTQPR	180
Db	121	LQAOVLSFQAYPTARCVLLEVQVPAALVQFGOSGVSVYDCFEAALGSEVRWSTQPR	180
Qy	181	YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEOHFGLSLYWNQVQGPGRWHKNT	240
Db	181	YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEOHFGLSLYWNQVQGPGRWHKNT	240
Qy	241	GPQIITLNTDLVPCLCLOVWPLEPDSVRTNICPPREDPRAHONLWQAARLLTLQSWL	300
Db	241	GPQIITLNTDLVPCLCLOVWPLEPDSVRTNICPPREDPRAHONLWQAARLLTLQSWL	300

QY 301 LDAPCSLPAEAAALCWAPGDCQPLVPPLSWENVTVDKLVLEFPPLKAGHPNLCVQVNSSE 360
Db 301 LDAPCSLPAEAAALCWAPGDCQPLVPPLSWENVTVDKLVLEFPPLKAGHPNLCVQVNSSE 360
QY 361 KLQQLCEWLADSLGPKDDVLLLETRGPQDNRSICALPESGCTSLPSKASTRAARLGEYL 420
Db 361 KLQQLCEWLADSLGPKDDVLLLETRGPQDNRSICALPESGCTSLPSKASTRAARLGEYL 420
QY 421 LDQLSQGCQLQWDDDLGALWACPMOKYIHKRWALVWLACLLFAAALSLILLKKDHAKA 480
Db 421 LDQLSQGCQLQWDDDLGALWACPMOKYIHKRWALVWLACLLFAAALSLILLKKDHAKA 480
QY 481 AARGRAALLYSADDSGFERLVCALASALCOLPLRVAVDWLWSRRELSAQGPVAFHQAQR 540
Db 481 AARGRAALLYSADDSGFERLVCALASALCOLPLRVAVDWLWSRRELSAQGPVAFHQAQR 540
QY 541 QTLQEGVVVLLFSPGAVLCSWLODGVSGPGAHGPHDAFRASLSVLPDFLOGRAPGS 600
Db 541 QTLQEGVVVLLFSPGAVLCSWLODGVSGPGAHGPHDAFRASLSVLPDFLOGRAPGS 600
QY 601 YVGACFDRLHDPDAVPALFRTVPVFTLPSQLPDFLGALQOPRPRSGRLQERAEQVSRAL 660
Db 601 YVGACFDRLHDPDAVPALFRTVPVFTLPSQLPDFLGALQOPRPRSGRLQERAEQVSRAL 660
QY 661 QPALDSYFHPGTPAPGRGVGPGAGGAGDGT 692
Db 661 QPALDSYFHPGTPAPGRGVGPGAGGAGDGT 692

RESULT 2
US-09-874-503-14
; Sequence 14, Application US/09874503
; Patent No. US20020177188A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah G.
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovasnik, Melissa A.
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P3(US)
; CURRENT APPLICATION NUMBER: US/09/874,503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/244,072
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/213,807
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/138,387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: US 60/134,287

; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/131,022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: US 60/130,232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/113,621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-20
; PRIOR APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/380,142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: US 09/380,138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 14
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-874-503-14

Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

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Db 1 MPVPWFLLSLALGRSPVVLRLVGPQDATHCSFGLSCLRLWDSIDLCLPGLDVPAPGPV 60
QY 61 LAPTHLQTELVLRCOKETDCDLCLRVAVHLVHGHWEPEDEKFGGAADSGVEEPRNAS 120
Db 61 LAPTHLQTELVLRCOKETDCDLCLRVAVHLVHGHWEPEDEKFGGAADSGVEEPRNAS 120
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Db 121 LQAQVVLVSFQAYPTARCVCVLELVQVFAALVQFGQSGVSVYDCFEAALGSEVRITWSTQPR 180

QY 181 YEKELNHTQOLPALPWLNVSDGDNVHLVNLVNSEBQHFGSLYWNQVQPPKPRWHKNLT 240
Db 181 YEKELNHTQOLPALPWLNVSDGDNVHLVNLVNSEBQHFGSLYWNQVQPPKPRWHKNLT 240
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Db 241 GPQIITLNTHTDLVPCLCIQVNPPLSDSVRTNICPPREDPRAHONLWQAARLRLTLQSWL 300
QY 301 LDAPCSLPAEALCWAPGDCOPPLVPPLSWENVTVDKVLKGNPCLVCVQVNSSE 360
Db 301 LDAPCSLPAEALCWAPGDCOPPLVPPLSWENVTVDKVLKGNPCLVCVQVNSSE 360
QY 361 KLQLOECILWADSLGPKLDVLLLETRGPQDNRSICALPEPGCTSLPSKASTRAARLGEYL 420
Db 361 KLQLOECILWADSLGPKLDVLLLETRGPQDNRSICALPEPGCTSLPSKASTRAARLGEYL 420
QY 421 LQDLSQGCILQWLDDDLGALWACPMCKYIHKRWALVWLACLLFAALSLILLLKKDHAK - 479
Db 421 LQDLSQGCILQWLDDDLGALWACPMCKYIHKRWALVWLACLLFAALSLILLLKKDHAKG 480
QY 480 -----AAARGAALLLSADSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
Db 481 WLRLLLKQDVRSGAARGAALLLSADSGFERLVGALASALCQLPLRVAVDLWSRRELS 540
QY 528 AOGPVAFHQAORQTLQEGGVVWLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
Db 541 AOGPVAFHQAORQTLQEGGVVWLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600
QY 588 VLPDFLQGRAGSVGVGACFDRLLHPDAPVALFRVVPVFTLPSQLPDFLQALQOQPRAPRS 647
Db 601 VLPDFLQGRAGSVGVGACFDRLLHPDAPVALFRVVPVFTLPSQLPDFLQALQOQPRAPRS 660
QY 648 RLQERAEQVSRAALQALDLSYFHPGTPAGRGVGVGAGPGAGDGT 692
Db 661 RLQERAEQVSRAALQALDLSYFHPGTPAGRGVGVGAGPGAGDGT 705

RESULT 3
US-10-000-157-14
; Sequence 14, Application US/10000157
; Publication No. US20020182673A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul L.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovasnik, Melissa.
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Collin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P4(US)
; CURRENT APPLICATION NUMBER: US/10/000,157
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26

; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/172096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/175481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/213807
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/242837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/244072
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/253646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/908827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/931836
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692

;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/21066
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: PCT/US01/21735
;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 39
;; SEQ ID NO 14
;; LENGTH: 705
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-000-157-14

Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 MPVPFLLSLALGRSPVLSRLVGPQDATHCSPGLSCLRLWSDIILCLPGDIVPAPGV 60
DB 1 MPVPFLLSLALGRSPVLSRLVGPQDATHCSPGLSCLRLWSDIILCLPGDIVPAPGV 60
QY 61 LAPTHLQTELVLRCOKETDCDLCLRVAVHLAVHGHWEPEDEEKGGAADSGVEEPRNAS 120
DB 61 LAPTHLQTELVLRCOKETDCDLCLRVAVHLAVHGHWEPEDEEKGGAADSGVEEPRNAS 120
QY 121 LQAQVLSFQAYPTARCVLLEQVPAALVQFGQSVGVYDCFEAALGSEVRWISYTOPR 180
DB 121 LQAQVLSFQAYPTARCVLLEQVPAALVQFGQSVGVYDCFEAALGSEVRWISYTOPR 180
QY 181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEQHFGLSLYWNQVQGPCKPRWHKNT 240
DB 181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEQHFGLSLYWNQVQGPCKPRWHKNT 240
QY 241 GPOIITLNTHTDLVPCLCIQVWPLEPDSVRTNICPPREDPRAHONLWQARLLTLQSWL 300
DB 241 GPOIITLNTHTDLVPCLCIQVWPLEPDSVRTNICPPREDPRAHONLWQARLLTLQSWL 300
QY 301 LDAPCSLPAEALCWRAFGDPCQPLVPPLSWENVTVDKLEFPLKKGHPNLCVQVNSSE 360
DB 301 LDAPCSLPAEALCWRAFGDPCQPLVPPLSWENVTVDKLEFPLKKGHPNLCVQVNSSE 360
QY 361 KLQLOECLWADSLGPKDDVLLLETRGPQDNRSCLALEPSGCTSLPSKASTRAARLGEYL 420
DB 361 KLQLOECLWADSLGPKDDVLLLETRGPQDNRSCLALEPSGCTSLPSKASTRAARLGEYL 420
QY 421 LQDLSGQCLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSILLKKDHAK - 479
DB 421 LQDLSGQCLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSILLKKDHAK 480
QY 480 -----AAARGAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 527
DB 481 WLRLKQDVRSGAARGAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 540
QY 528 AQGPVAMFHAORRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGGPHDAFRASLSC 587
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QY 588 VLPDFLOGRAGPSYVACFDRLHHPDAVPALFRTVPVFTLPQLPDLFALQOAPRPSG 647
DB 601 VLPDFLOGRAGPSYVACFDRLHHPDAVPALFRTVPVFTLPQLPDLFALQOAPRPSG 660
QY 648 RLQERAEQVSRLQALPDLSDYFHPGCTPAPGRGVGPGAGGAGDGT 692
DB 661 RLQERAEQVSRLQALPDLSDYFHPGCTPAPGRGVGPGAGGAGDGT 705

RESULT 4

US-10-063-547-162
;; Sequence 162, Application US/10063547
;; Publication No. US20020182638A1
;; GENERAL INFORMATION:
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gerritsen, Mary E.

;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3230R1C1
;; CURRENT APPLICATION NUMBER: US/10/063,547
;; CURRENT FILING DATE: 2002-05-02
;; Prior Application removed - See File Wrapper or Palm
;; NUMBER OF SEQ ID NOS: 170
;; SEQ ID NO 162
;; LENGTH: 705
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-063-547-162

Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 MPVPFLLSLALGRSPVLSRLVGPQDATHCSPGLSCLRLWSDIILCLPGDIVPAPGV 60
DB 1 MPVPFLLSLALGRSPVLSRLVGPQDATHCSPGLSCLRLWSDIILCLPGDIVPAPGV 60
QY 61 LAPTHLQTELVLRCOKETDCDLCLRVAVHLAVHGHWEPEDEEKGGAADSGVEEPRNAS 120
DB 61 LAPTHLQTELVLRCOKETDCDLCLRVAVHLAVHGHWEPEDEEKGGAADSGVEEPRNAS 120
QY 121 LQAQVLSFQAYPTARCVLLEQVPAALVQFGQSVGVYDCFEAALGSEVRWISYTOPR 180
DB 121 LQAQVLSFQAYPTARCVLLEQVPAALVQFGQSVGVYDCFEAALGSEVRWISYTOPR 180
QY 181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEQHFGLSLYWNQVQGPCKPRWHKNT 240
DB 181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEQHFGLSLYWNQVQGPCKPRWHKNT 240
QY 241 GPOIITLNTHTDLVPCLCIQVWPLEPDSVRTNICPPREDPRAHONLWQARLLTLQSWL 300
DB 241 GPOIITLNTHTDLVPCLCIQVWPLEPDSVRTNICPPREDPRAHONLWQARLLTLQSWL 300
QY 301 LDAPCSLPAEALCWRAFGDPCQPLVPPLSWENVTVDKLEFPLKKGHPNLCVQVNSSE 360
DB 301 LDAPCSLPAEALCWRAFGDPCQPLVPPLSWENVTVDKLEFPLKKGHPNLCVQVNSSE 360
QY 361 KLQLOECLWADSLGPKDDVLLLETRGPQDNRSCLALEPSGCTSLPSKASTRAARLGEYL 420
DB 361 KLQLOECLWADSLGPKDDVLLLETRGPQDNRSCLALEPSGCTSLPSKASTRAARLGEYL 420
QY 421 LQDLSGQCLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSILLKKDHAK - 479
DB 421 LQDLSGQCLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSILLKKDHAK 480
QY 480 -----AAARGAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 527
DB 481 WLRLKQDVRSGAARGAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 540
QY 528 AQGPVAMFHAORRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGGPHDAFRASLSC 587
DB 541 AQGPVAMFHAORRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGGPHDAFRASLSC 600
QY 588 VLPDFLOGRAGPSYVACFDRLHHPDAVPALFRTVPVFTLPQLPDLFALQOAPRPSG 647
DB 601 VLPDFLOGRAGPSYVACFDRLHHPDAVPALFRTVPVFTLPQLPDLFALQOAPRPSG 660
QY 648 RLQERAEQVSRLQALPDLSDYFHPGCTPAPGRGVGPGAGGAGDGT 692
DB 661 RLQERAEQVSRLQALPDLSDYFHPGCTPAPGRGVGPGAGGAGDGT 705

RESULT 5

US-09-816-744-14
; Sequence 14, Application US/09816744
; Publication No. US20030003546A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381RIC1P2(US)
; CURRENT APPLICATION NUMBER: US/09/816,744
; CURRENT FILING DATE: 2001-03-22
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 14
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-816-744-14

Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 MPVPFLLSLALGRSPVLSRLVGPQDATHCGSPGLSCRLWSDIILCLPGDIVPAGPV 60
DB 1 MPVPFLLSLALGRSPVLSRLVGPQDATHCGSPGLSCRLWSDIILCLPGDIVPAGPV 60
QY 61 LAPTHLOTLVLCQKETDCILRVAVHLAVHCHWEEPEDEEFKGAADSGVEEPRNAS 120
DB 61 LAPTHLOTLVLCQKETDCILRVAVHLAVHCHWEEPEDEEFKGAADSGVEEPRNAS 120
QY 121 LQAQVVLFSQAYTARCVLLEVVQPAALVQFGQSVGVVYDCEFAALGSEVRIWSYQPR 180
DB 121 LQAQVVLFSQAYTARCVLLEVVQPAALVQFGQSVGVVYDCEFAALGSEVRIWSYQPR 180
QY 181 YEKELNHTQOLPALPWLNVNSADGDNVHLVNVSEEQHFGLSLYWNQYOGPPKPRHKNLT 240
DB 181 YEKELNHTQOLPALPWLNVNSADGDNVHLVNVSEEQHFGLSLYWNQYOGPPKPRHKNLT 240
QY 241 GPQITLNTHTDLVPCLCIQWPLEPSVRTNICPFREDPRAHQNLMQAAARLLTLQSWL 300
DB 241 GPQITLNTHTDLVPCLCIQWPLEPSVRTNICPFREDPRAHQNLMQAAARLLTLQSWL 300
QY 301 LDAPCSLPAEALCWAPGDCQCPVPLPSWENVTVDKVLEFPLKLGHNLCVQVNSSE 360
DB 301 LDAPCSLPAEALCWAPGDCQCPVPLPSWENVTVDKVLEFPLKLGHNLCVQVNSSE 360
QY 361 KIQLQECUWADSLGPLKDDVLLLETRGPQDNRSICALEPSGCTSLPSKASTRAARLGEYL 420
DB 361 KIQLQECUWADSLGPLKDDVLLLETRGPQDNRSICALEPSGCTSLPSKASTRAARLGEYL 420
QY 421 LQDLQSGQCQLQWDDDLGALWACPMQDKYTHKRWALVWLACLLFAAALLSLLLKDKHAK - 479
DB 421 LQDLQSGQCQLQWDDDLGALWACPMQDKYTHKRWALVWLACLLFAAALLSLLLKDKHAKG 480
QY 480 -----AAARGRAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 527
DB 481 WLRLKQDVRSAAARGRAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 540
QY 528 AOGPVAFWFAORRQTLQEGGVVLLFSPGAVALCSEWLQDVGSGGAGHGHDAFRASLSC 587

DB 541 AOGPVAFWFAORRQTLQEGGVVLLFSPGAVALCSEWLQDVGSGGAGHGHDAFRASLSC 600
QY 588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDLFGLAQOQPRAPRSG 647
DB 601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDLFGLAQOQPRAPRSG 660
QY 648 RLQERAEQVSRALQALPDLSDYFHPPTAPGRGVGPGAGPGAGDGT 692
DB 661 RLQERAEQVSRALQALPDLSDYFHPPTAPGRGVGPGAGPGAGDGT 705

RESULT 6

US-09-747-259-14
; Sequence 14, Application US/09747259
; Publication No. US20030008815A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381RIC1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 14
; LENGTH: 705

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; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-747-259-14

Query Match          99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 MPVPWFLSLALGRSPVVLRLVGPQDATHCSPGLSCRLWDSDIICLPDGIIVPAGPV 60
    |||||
Db 1 MPVPWFLSLALGRSPVVLRLVGPQDATHCSPGLSCRLWDSDIICLPDGIIVPAGPV 60

QY 61 LAPTHLOTELVLRCQKEDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120
    |||||
Db 61 LAPTHLOTELVLRCQKEDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120

QY 121 LQAQVVLVSFOAYPTARCVLLEVOVPAALVQFGSGVGVYDCFEAALGSEVRIWSYTPR 180
    |||||
Db 121 LQAQVVLVSFOAYPTARCVLLEVOVPAALVQFGSGVGVYDCFEAALGSEVRIWSYTPR 180

QY 181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEEQHFGLSLYWNOVGQPKPRHKNLT 240
    |||||
Db 181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEEQHFGLSLYWNOVGQPKPRHKNLT 240

QY 241 GPQIITLNHTDLVPCICIQWVPLEPDSVRTNICPFREDPRAHQLWQAARLLLTLSWL 300
    |||||
Db 241 GPQIITLNHTDLVPCICIQWVPLEPDSVRTNICPFREDPRAHQLWQAARLLLTLSWL 300

QY 301 LDAPCSLPAEALCWAPAGGDCQPLVPLSWENVTVDKVLEFPPLKGHPNLCVQVNSSE 360
    |||||
Db 301 LDAPCSLPAEALCWAPAGGDCQPLVPLSWENVTVDKVLEFPPLKGHPNLCVQVNSSE 360

QY 361 KLQLOEQLWADSLGPKDDVLLLETRGPQDNRSICALPESGCTSLPSKASTRAARLGEYL 420
    |||||
Db 361 KLQLOEQLWADSLGPKDDVLLLETRGPQDNRSICALPESGCTSLPSKASTRAARLGEYL 420

QY 421 LQDLSGGCQLQWDDDLGALWACPMDKYTHKRWALVWLACLLFAAALSLLILLKKDHAK - 479
    |||||
Db 421 LQDLSGGCQLQWDDDLGALWACPMDKYTHKRWALVWLACLLFAAALSLLILLKKDHAK - 479

QY 480 -----AARGRAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 527
    |||||
Db 480 -----AARGRAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 527

QY 528 AQGPVAFHAQRROTLOEGGVVLLFSPGAVALCSEWLQDGVSGPGAGHGHDFRSLSC 587
    |||||
Db 528 AQGPVAFHAQRROTLOEGGVVLLFSPGAVALCSEWLQDGVSGPGAGHGHDFRSLSC 587

QY 541 AQGPVAFHAQRROTLOEGGVVLLFSPGAVALCSEWLQDGVSGPGAGHGHDFRSLSC 600
    |||||
Db 541 AQGPVAFHAQRROTLOEGGVVLLFSPGAVALCSEWLQDGVSGPGAGHGHDFRSLSC 600

QY 588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGLAQOPRPRSG 647
    |||||
Db 588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGLAQOPRPRSG 647

QY 601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGLAQOPRPRSG 660
    |||||
Db 601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGLAQOPRPRSG 660

QY 648 RLQERAEQVSRLQALPDLDSYFHPGTPAPGRGVGPGAGGAGDGT 692
    |||||
Db 648 RLQERAEQVSRLQALPDLDSYFHPGTPAPGRGVGPGAGGAGDGT 692

QY 661 RLQERAEQVSRLQALPDLDSYFHPGTPAPGRGVGPGAGGAGDGT 705
    |||||
Db 661 RLQERAEQVSRLQALPDLDSYFHPGTPAPGRGVGPGAGGAGDGT 705

RESULT 7
US-10-174-590-598
; Sequence 598, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 598
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-598

Query Match          99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 MPVPWFLSLALGRSPVVLRLVGPQDATHCSPGLSCRLWDSDIICLPDGIIVPAGPV 60
    |||||
Db 1 MPVPWFLSLALGRSPVVLRLVGPQDATHCSPGLSCRLWDSDIICLPDGIIVPAGPV 60

QY 61 LAPTHLOTELVLRCQKEDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120
    |||||
Db 61 LAPTHLOTELVLRCQKEDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120

QY 121 LQAQVVLVSFOAYPTARCVLLEVOVPAALVQFGSGVGVYDCFEAALGSEVRIWSYTPR 180
    |||||
Db 121 LQAQVVLVSFOAYPTARCVLLEVOVPAALVQFGSGVGVYDCFEAALGSEVRIWSYTPR 180

QY 181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEEQHFGLSLYWNOVGQPKPRHKNLT 240
    |||||
Db 181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEEQHFGLSLYWNOVGQPKPRHKNLT 240

QY 241 GPQIITLNHTDLVPCICIQWVPLEPDSVRTNICPFREDPRAHQLWQAARLLLTLSWL 300
    |||||
Db 241 GPQIITLNHTDLVPCICIQWVPLEPDSVRTNICPFREDPRAHQLWQAARLLLTLSWL 300

QY 301 LDAPCSLPAEALCWAPAGGDCQPLVPLSWENVTVDKVLEFPPLKGHPNLCVQVNSSE 360
    |||||
Db 301 LDAPCSLPAEALCWAPAGGDCQPLVPLSWENVTVDKVLEFPPLKGHPNLCVQVNSSE 360

QY 361 KLQLOEQLWADSLGPKDDVLLLETRGPQDNRSICALPESGCTSLPSKASTRAARLGEYL 420
    |||||
Db 361 KLQLOEQLWADSLGPKDDVLLLETRGPQDNRSICALPESGCTSLPSKASTRAARLGEYL 420

QY 421 LQDLSGGCQLQWDDDLGALWACPMDKYTHKRWALVWLACLLFAAALSLLILLKKDHAK - 479
    |||||
Db 421 LQDLSGGCQLQWDDDLGALWACPMDKYTHKRWALVWLACLLFAAALSLLILLKKDHAK - 479

QY 480 -----AARGRAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 527
    |||||
Db 480 -----AARGRAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 527

QY 528 AQGPVAFHAQRROTLOEGGVVLLFSPGAVALCSEWLQDGVSGPGAGHGHDFRSLSC 587
    |||||
Db 528 AQGPVAFHAQRROTLOEGGVVLLFSPGAVALCSEWLQDGVSGPGAGHGHDFRSLSC 587

QY 541 AQGPVAFHAQRROTLOEGGVVLLFSPGAVALCSEWLQDGVSGPGAGHGHDFRSLSC 600
    |||||
Db 541 AQGPVAFHAQRROTLOEGGVVLLFSPGAVALCSEWLQDGVSGPGAGHGHDFRSLSC 600

QY 588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGLAQOPRPRSG 647
    |||||
Db 588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGLAQOPRPRSG 647

QY 601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGLAQOPRPRSG 660
    |||||
Db 601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGLAQOPRPRSG 660

QY 648 RLQERAEQVSRLQALPDLDSYFHPGTPAPGRGVGPGAGGAGDGT 692
    |||||
Db 648 RLQERAEQVSRLQALPDLDSYFHPGTPAPGRGVGPGAGGAGDGT 692

QY 661 RLQERAEQVSRLQALPDLDSYFHPGTPAPGRGVGPGAGGAGDGT 705
    |||||
Db 661 RLQERAEQVSRLQALPDLDSYFHPGTPAPGRGVGPGAGGAGDGT 705

RESULT 8
US-10-176-758-598
; Sequence 598, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
```

APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430RIC104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 598
LENGTH: 705
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-758-598

Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 MPVPFLLSLALGRSPVLSRLERLVGPQDATHCSPGLSCLRLWDSIDLCLPGDIVPAPGPV 60
Db 1 MPVPFLLSLALGRSPVLSRLERLVGPQDATHCSPGLSCLRLWDSIDLCLPGDIVPAPGPV 60

Qy 61 LAPTHLOTLELVLCRKQETDCDCLRVAVHLAVHGHWEPEDEKFGGAADSGVEEPRNAS 120
Db 61 LAPTHLOTLELVLCRKQETDCDCLRVAVHLAVHGHWEPEDEKFGGAADSGVEEPRNAS 120

Qy 121 LQAQVVLVSFOAYPTARCVLLEQVPAALVQFGSGVSVYDCFEAALGSEVRINSYQTPR 180
Db 121 LQAQVVLVSFOAYPTARCVLLEQVPAALVQFGSGVSVYDCFEAALGSEVRINSYQTPR 180

Qy 181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEEHFGLSLYWNQVQGGPKPRWHKNTL 240
Db 181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEEHFGLSLYWNQVQGGPKPRWHKNTL 240

Qy 241 GPQIITLNTHTDLVPCLCIQWPLEPDSVRTNICPFREDPRAHQNLMQAAARLLTLQSWL 300
Db 241 GPQIITLNTHTDLVPCLCIQWPLEPDSVRTNICPFREDPRAHQNLMQAAARLLTLQSWL 300

Qy 301 LDAPCSLPAEALCWAPGDDPCQPLVPPPLSWENVTVDKVLFPPLKGHNPCLVQVNSSE 360
Db 301 LDAPCSLPAEALCWAPGDDPCQPLVPPPLSWENVTVDKVLFPPLKGHNPCLVQVNSSE 360

Qy 361 KLQLOECLWADSLGPKDDVLLLETRGPQDNRSCLALEPSGCTSLPSKASTRAARLGEYL 420
Db 361 KLQLOECLWADSLGPKDDVLLLETRGPQDNRSCLALEPSGCTSLPSKASTRAARLGEYL 420

Qy 421 LQDLOGGOCLOLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLLILLKKDHAK - 479
Db 421 LQDLOGGOCLOLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLLILLKKDHAK 480

Qy 480 -----AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
Db 481 WLRLKQDVRSGAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy 528 AQGPVAFHQAORROTLOEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
Db 541 AQGPVAFHQAORROTLOEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy 588 VLPDFLOGRAPGSYVGACFDRLHLHPDAVPALFRTVPVFTLPQOLPDLGALQOPRAPRSG 647
Db 601 VLPDFLOGRAPGSYVGACFDRLHLHPDAVPALFRTVPVFTLPQOLPDLGALQOPRAPRSG 660

Qy 648 RLOERAEOVSRALQALPDYSYFHPGTPAPGRGVGPGAGGAGDGT 692
Db 661 RLOERAEOVSRALQALPDYSYFHPGTPAPGRGVGPGAGGAGDGT 705

RESULT 9
US-10-063-616-162
Sequence 162, Application US/10063616
Publication No. US20030013855A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230RIC1
CURRENT APPLICATION NUMBER: US/10/063,616
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 162
LENGTH: 705
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-616-162

Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 MPVPFLLSLALGRSPVLSRLERLVGPQDATHCSPGLSCLRLWDSIDLCLPGDIVPAPGPV 60
Db 1 MPVPFLLSLALGRSPVLSRLERLVGPQDATHCSPGLSCLRLWDSIDLCLPGDIVPAPGPV 60

Qy 61 LAPTHLOTLELVLCRKQETDCDCLRVAVHLAVHGHWEPEDEKFGGAADSGVEEPRNAS 120
Db 61 LAPTHLOTLELVLCRKQETDCDCLRVAVHLAVHGHWEPEDEKFGGAADSGVEEPRNAS 120

Qy 121 LQAQVVLVSFOAYPTARCVLLEQVPAALVQFGSGVSVYDCFEAALGSEVRINSYQTPR 180
Db 121 LQAQVVLVSFOAYPTARCVLLEQVPAALVQFGSGVSVYDCFEAALGSEVRINSYQTPR 180

Qy 181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEEHFGLSLYWNQVQGGPKPRWHKNTL 240
Db 181 YEKELNHTQQLPALPWLNVSDGDNVHLVNVSEEHFGLSLYWNQVQGGPKPRWHKNTL 240

Qy 241 GPQIITLNTHTDLVPCLCIQWPLEPDSVRTNICPFREDPRAHQNLMQAAARLLTLQSWL 300
Db 241 GPQIITLNTHTDLVPCLCIQWPLEPDSVRTNICPFREDPRAHQNLMQAAARLLTLQSWL 300

Qy 301 LDAPCSLPAEALCWAPGDDPCQPLVPPPLSWENVTVDKVLFPPLKGHNPCLVQVNSSE 360
Db 301 LDAPCSLPAEALCWAPGDDPCQPLVPPPLSWENVTVDKVLFPPLKGHNPCLVQVNSSE 360

Qy 361 KLQLOECLWADSLGPKDDVLLLETRGPQDNRSCLALEPSGCTSLPSKASTRAARLGEYL 420
Db 361 KLQLOECLWADSLGPKDDVLLLETRGPQDNRSCLALEPSGCTSLPSKASTRAARLGEYL 420

Qy 421 LQDLOGGOCLOLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLLILLKKDHAK - 479
Db 421 LQDLOGGOCLOLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLLILLKKDHAK 480

Qy 480 -----AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
Db 481 WLRLKQDVRSGAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy 528 AQGPVAFHQAORROTLOEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
Db 541 AQGPVAFHQAORROTLOEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

QY 588 VLPDFLQGRAPGSYVACGDFRLLHPDAVPALFRTVPVFTLPSQLPDFLQALQOPRPRSG 647
|||||
Db 601 VLPDFLQGRAPGSYVACGDFRLLHPDAVPALFRTVPVFTLPSQLPDFLQALQOPRPRSG 660
QY 648 RLQERAEQVSRLQALPDLSDYFHPGTPAPGRGVGPGAGGAGDGT 692
|||||
Db 661 RLQERAEQVSRLQALPDLSDYFHPGTPAPGRGVGPGAGGAGDGT 705

RESULT 10

US-10-175-737-598
; Sequence 598, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowsky, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-08-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 598
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-598

Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 MPVPWFLLSLALGRSPVVLRLVGPQDATHCSFGLSCLRLWDSIDLCLPGDIVPAPGPV 60
Db 1 MPVPWFLLSLALGRSPVVLRLVGPQDATHCSFGLSCLRLWDSIDLCLPGDIVPAPGPV 60
QY 61 LAPHLOTELVLRCQKETDCDCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120
Db 61 LAPHLOTELVLRCQKETDCDCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120
QY 121 LQAOVVLVSFOAYPTARCVLLEVOVPAALVQFGSQSVGVVYDCFEAALGSEVRINWSTQPR 180
Db 121 LQAOVVLVSFOAYPTARCVLLEVOVPAALVQFGSQSVGVVYDCFEAALGSEVRINWSTQPR 180
QY 181 YEKELNHTQOLPALPWLNVSDGDNVHLVNLVNSEQHFGLSLYWNVOGPPKPRWHKNTL 240
Db 181 YEKELNHTQOLPALPWLNVSDGDNVHLVNLVNSEQHFGLSLYWNVOGPPKPRWHKNTL 240
QY 241 GPOIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHONLWQAARLLTLQSWL 300
Db 241 GPOIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHONLWQAARLLTLQSWL 300
QY 301 LDAPCSLPAEALCWAPGDPQCPVLPPLSWENVTVDKVFLEPFLKHPNLCVQVNSSE 360
Db 301 LDAPCSLPAEALCWAPGDPQCPVLPPLSWENVTVDKVFLEPFLKHPNLCVQVNSSE 360
QY 361 KLQLOECLWADSLGPKDDVLLLETRGPDNRSLCALEPSCGCTSLPSKASTRAARLGEYL 420
Db 361 KLQLOECLWADSLGPKDDVLLLETRGPDNRSLCALEPSCGCTSLPSKASTRAARLGEYL 420
QY 421 LQDLSQGCQLQDMDLGLWACPMCKYIHKRWALVWLACLLFAAALSILLKKDHAK - 479
Db 421 LQDLSQGCQLQDMDLGLWACPMCKYIHKRWALVWLACLLFAAALSILLKKDHAK - 480

QY 480 -----AAARGRAALLLYSADDSGFERLYGALASALCOLPLRVAVDLWSRRELS 527
|||||
Db 481 WURLLKQDVRSGAAARGRAALLLYSADDSGFERLYGALASALCOLPLRVAVDLWSRRELS 540
QY 528 AGGPVAFWFAHQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGYSGPGAHGPHDAFRASLSC 587
|||||
Db 541 AGGPVAFWFAHQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGYSGPGAHGPHDAFRASLSC 600
QY 588 VLPDFLQGRAPGSYVACGDFRLLHPDAVPALFRTVPVFTLPSQLPDFLQALQOPRPRSG 647
|||||
Db 601 VLPDFLQGRAPGSYVACGDFRLLHPDAVPALFRTVPVFTLPSQLPDFLQALQOPRPRSG 660
QY 648 RLQERAEQVSRLQALPDLSDYFHPGTPAPGRGVGPGAGGAGDGT 692
|||||
Db 661 RLQERAEQVSRLQALPDLSDYFHPGTPAPGRGVGPGAGGAGDGT 705

RESULT 11

US-10-063-502-162
; Sequence 162, Application US/10063502
; Publication No. US20030023042A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,502
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 162
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-502-162

Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 MPVPWFLLSLALGRSPVVLRLVGPQDATHCSFGLSCLRLWDSIDLCLPGDIVPAPGPV 60
Db 1 MPVPWFLLSLALGRSPVVLRLVGPQDATHCSFGLSCLRLWDSIDLCLPGDIVPAPGPV 60
QY 61 LAPHLOTELVLRCQKETDCDCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120
Db 61 LAPHLOTELVLRCQKETDCDCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120
QY 121 LQAOVVLVSFOAYPTARCVLLEVOVPAALVQFGSQSVGVVYDCFEAALGSEVRINWSTQPR 180
Db 121 LQAOVVLVSFOAYPTARCVLLEVOVPAALVQFGSQSVGVVYDCFEAALGSEVRINWSTQPR 180
QY 181 YEKELNHTQOLPALPWLNVSDGDNVHLVNLVNSEQHFGLSLYWNVOGPPKPRWHKNTL 240
Db 181 YEKELNHTQOLPALPWLNVSDGDNVHLVNLVNSEQHFGLSLYWNVOGPPKPRWHKNTL 240
QY 241 GPOIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHONLWQAARLLTLQSWL 300
Db 241 GPOIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHONLWQAARLLTLQSWL 300
QY 301 LDAPCSLPAEALCWAPGDPQCPVLPPLSWENVTVDKVFLEPFLKHPNLCVQVNSSE 360
Db 301 LDAPCSLPAEALCWAPGDPQCPVLPPLSWENVTVDKVFLEPFLKHPNLCVQVNSSE 360

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QY 361 KLOQECLWADSLGPKDDVLLLETRGPQDNRSICALPSGCTSLPSKASTRAARLGEYL 420
|||||
Db 361 KLOQECLWADSLGPKDDVLLLETRGPQDNRSICALPSGCTSLPSKASTRAARLGEYL 420
|||||
QY 421 LQDLSQGCQLQWDDDLGALWACPMCKYIHKRWALVWLACILFAAALSILLLKKDHAK - 479
|||||
Db 421 LQDLSQGCQLQWDDDLGALWACPMCKYIHKRWALVWLACILFAAALSILLLKKDHAKG 480
|||||
QY 480 -----AAARGAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
|||||
Db 481 WLRLKKQDVRSGAAARGAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540
|||||
QY 528 AOGPVAMFHAQRQTLOEGGVVLLFSPGAVALCSEWLQDVGSGAGHGDHAFRASLSC 587
|||||
Db 541 AOGPVAMFHAQRQTLOEGGVVLLFSPGAVALCSEWLQDVGSGAGHGDHAFRASLSC 600
|||||
QY 588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRVVPVFTLPSQLPDFLQALQOOPRPSG 647
|||||
Db 601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRVVPVFTLPSQLPDFLQALQOOPRPSG 660
|||||
QY 648 RLQERAEQVSRAALQALDLSYFHPGTPAPGRGVGPGAGGAGDGT 692
|||||
Db 661 RLQERAEQVSRAALQALDLSYFHPGTPAPGRGVGPGAGGAGDGT 705
|||||

RESULT 12
US-10-173-706-598
; Sequence 598, Application US/10173706
; Publication No. US2003002293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 598
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-598
```

```
Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
```

```
QY 1 MPVPWFLLSALGRSPVVLSERLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAPGPV 60
|||||
Db 1 MPVPWFLLSALGRSPVVLSERLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAPGPV 60
|||||
QY 61 LAPTHLQTELVLRCOKETDCDCLRVAVHLAVHGWEEPEDEEKFGGAADSGVVEEPNRS 120
|||||
Db 61 LAPTHLQTELVLRCOKETDCDCLRVAVHLAVHGWEEPEDEEKFGGAADSGVVEEPNRS 120
|||||
QY 121 LQAQVVLFSQAYPTARCVLLEQVPAALVQFGSGSVVYDCFEAALGSEVRITWSYTOPR 180
|||||
Db 121 LQAQVVLFSQAYPTARCVLLEQVPAALVQFGSGSVVYDCFEAALGSEVRITWSYTOPR 180
|||||
QY 181 YEKELNHTQQLPALPWLNVSDGDNVHLVLYNSEQHFGLSLYWNQVQGPCKPRWHKNLT 240
|||||
Db 181 YEKELNHTQQLPALPWLNVSDGDNVHLVLYNSEQHFGLSLYWNQVQGPCKPRWHKNLT 240
|||||
```

```
QY 241 GPOIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLMQAAARLLTLQSWL 300
|||||
Db 241 GPOIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLMQAAARLLTLQSWL 300
|||||
QY 301 LDAPCSLPAAEALCWRAPGDPQCPPLPSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
|||||
Db 301 LDAPCSLPAAEALCWRAPGDPQCPPLPSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
|||||
QY 361 KLOQECLWADSLGPKDDVLLLETRGPQDNRSICALPSGCTSLPSKASTRAARLGEYL 420
|||||
Db 361 KLOQECLWADSLGPKDDVLLLETRGPQDNRSICALPSGCTSLPSKASTRAARLGEYL 420
|||||
QY 421 LQDLSQGCQLQWDDDLGALWACPMCKYIHKRWALVWLACILFAAALSILLLKKDHAK - 479
|||||
Db 421 LQDLSQGCQLQWDDDLGALWACPMCKYIHKRWALVWLACILFAAALSILLLKKDHAKG 480
|||||
QY 480 -----AAARGAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
|||||
Db 481 WLRLKKQDVRSGAAARGAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540
|||||
QY 528 AOGPVAMFHAQRQTLOEGGVVLLFSPGAVALCSEWLQDVGSGAGHGDHAFRASLSC 587
|||||
Db 541 AOGPVAMFHAQRQTLOEGGVVLLFSPGAVALCSEWLQDVGSGAGHGDHAFRASLSC 600
|||||
QY 588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRVVPVFTLPSQLPDFLQALQOOPRPSG 647
|||||
Db 601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRVVPVFTLPSQLPDFLQALQOOPRPSG 660
|||||
QY 648 RLQERAEQVSRAALQALDLSYFHPGTPAPGRGVGPGAGGAGDGT 692
|||||
Db 661 RLQERAEQVSRAALQALDLSYFHPGTPAPGRGVGPGAGGAGDGT 705
|||||
```

```
RESULT 13
US-10-175-738-598
; Sequence 598, Application US/10175738
; Publication No. US2003002294A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC45
; CURRENT APPLICATION NUMBER: US/10/175,738
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 598
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-738-598
```

```
Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
```

```
QY 1 MPVPWFLLSALGRSPVVLSERLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAPGPV 60
|||||
Db 1 MPVPWFLLSALGRSPVVLSERLVGPQDATHCSPGLSCLRWSDILCLPGDIVPAPGPV 60
|||||
QY 61 LAPTHLQTELVLRCOKETDCDCLRVAVHLAVHGWEEPEDEEKFGGAADSGVVEEPNRS 120
|||||
```


Db 61 LAPTHLOTELVLRCOKETDCDLCLRVAVHLAVHGHWEPEDEKFGGAADSGVEEPRNAS 120
QY 121 LQAOVVLVSFOAYPTARCVLLEVVQVPAALVQFGSGVSVYVDCFEAALGSEVRINWSTQPR 180
Db 121 LQAOVVLVSFOAYPTARCVLLEVVQVPAALVQFGSGVSVYVDCFEAALGSEVRINWSTQPR 180
QY 181 YEKELNHTQQLPALPWLNVNVSADGDNVHLVNVSEEQHFGLSLYWNQVQGPCKPRWHKNT 240
Db 181 YEKELNHTQQLPALPWLNVNVSADGDNVHLVNVSEEQHFGLSLYWNQVQGPCKPRWHKNT 240
QY 241 GPOIITLHNTDLVPCLCIQVWPLEPDSVTRNICPFREDPRAHQNLWQAARLLTLQSWL 300
Db 241 GPOIITLHNTDLVPCLCIQVWPLEPDSVTRNICPFREDPRAHQNLWQAARLLTLQSWL 300
QY 301 LDAPCSLPAEALCWRAFGDPCQPLVPLSWENVTVDKVLRLKLGHPNLCVQVNSSE 360
Db 301 LDAPCSLPAEALCWRAFGDPCQPLVPLSWENVTVDKVLRLKLGHPNLCVQVNSSE 360
QY 361 KLQQLCLWADSLGPKLDDVLLLETRGPDNRSICALPEPGCTSLPSKASTRAARLGEYL 420
Db 361 KLQQLCLWADSLGPKLDDVLLLETRGPDNRSICALPEPGCTSLPSKASTRAARLGEYL 420
QY 421 LQDLSGQCQLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLLILLKKDHAK - 479
Db 421 LQDLSGQCQLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLLILLKKDHAKG 480
QY 480 -----AAARGRAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 527
Db 481 WLRLKQDVRSAAARGRAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 540
QY 528 AOGPVAMFHAORRQTLQEGGVVLLFSPGAVALCSEWLQDVGSGPGAGHPDAFRASLSC 587
Db 541 AOGPVAMFHAORRQTLQEGGVVLLFSPGAVALCSEWLQDVGSGPGAGHPDAFRASLSC 600
QY 588 VLPDFLOGRAGPSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQOPRPRSG 647
Db 601 VLPDFLOGRAGPSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQOPRPRSG 660
QY 648 RLQERAEQVSRAEQALQALDSYFHPGTPAPGRGVGPGAGGAGDGT 692
Db 661 RLQERAEQVSRAEQALQALDSYFHPGTPAPGRGVGPGAGGAGDGT 705

RESULT 14
US-10-175-752-598
; Sequence 598, Application US/10175752
; Publication No. US2003002295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C60
; CURRENT APPLICATION NUMBER: US/10/175,752
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 598
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien

Query Match 99.6%; Score 3699.5; DB 9; Length 705;

US-10-175-752-598

Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
QY 1 MPVPWFLLSLALGRSPVLSRLERLVGPQDATHCSPGLSCLRLMDSILCLPGDIVPAGPV 60
Db 1 MPVPWFLLSLALGRSPVLSRLERLVGPQDATHCSPGLSCLRLMDSILCLPGDIVPAGPV 60
QY 61 LAPTHLOTELVLRCOKETDCDLCLRVAVHLAVHGHWEPEDEKFGGAADSGVEEPRNAS 120
Db 61 LAPTHLOTELVLRCOKETDCDLCLRVAVHLAVHGHWEPEDEKFGGAADSGVEEPRNAS 120
QY 121 LQAOVVLVSFOAYPTARCVLLEVVQVPAALVQFGSGVSVYVDCFEAALGSEVRINWSTQPR 180
Db 121 LQAOVVLVSFOAYPTARCVLLEVVQVPAALVQFGSGVSVYVDCFEAALGSEVRINWSTQPR 180
QY 181 YEKELNHTQQLPALPWLNVNVSADGDNVHLVNVSEEQHFGLSLYWNQVQGPCKPRWHKNT 240
Db 181 YEKELNHTQQLPALPWLNVNVSADGDNVHLVNVSEEQHFGLSLYWNQVQGPCKPRWHKNT 240
QY 241 GPOIITLHNTDLVPCLCIQVWPLEPDSVTRNICPFREDPRAHQNLWQAARLLTLQSWL 300
Db 241 GPOIITLHNTDLVPCLCIQVWPLEPDSVTRNICPFREDPRAHQNLWQAARLLTLQSWL 300
QY 301 LDAPCSLPAEALCWRAFGDPCQPLVPLSWENVTVDKVLRLKLGHPNLCVQVNSSE 360
Db 301 LDAPCSLPAEALCWRAFGDPCQPLVPLSWENVTVDKVLRLKLGHPNLCVQVNSSE 360
QY 361 KLQQLCLWADSLGPKLDDVLLLETRGPDNRSICALPEPGCTSLPSKASTRAARLGEYL 420
Db 361 KLQQLCLWADSLGPKLDDVLLLETRGPDNRSICALPEPGCTSLPSKASTRAARLGEYL 420
QY 421 LQDLSGQCQLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLLILLKKDHAK - 479
Db 421 LQDLSGQCQLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLLILLKKDHAKG 480
QY 480 -----AAARGRAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 527
Db 481 WLRLKQDVRSAAARGRAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELS 540
QY 528 AOGPVAMFHAORRQTLQEGGVVLLFSPGAVALCSEWLQDVGSGPGAGHPDAFRASLSC 587
Db 541 AOGPVAMFHAORRQTLQEGGVVLLFSPGAVALCSEWLQDVGSGPGAGHPDAFRASLSC 600
QY 588 VLPDFLOGRAGPSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQOPRPRSG 647
Db 601 VLPDFLOGRAGPSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQOPRPRSG 660
QY 648 RLQERAEQVSRAEQALQALDSYFHPGTPAPGRGVGPGAGGAGDGT 692
Db 661 RLQERAEQVSRAEQALQALDSYFHPGTPAPGRGVGPGAGGAGDGT 705

RESULT 15

US-10-176-482-598
; Sequence 598, Application US/10176482
; Publication No. US2003002296A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C70
; CURRENT APPLICATION NUMBER: US/10/176,482
; CURRENT FILING DATE: 2002-06-20


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; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 598
; LENGTH: 705
; TYPE: prt
; ORGANISM: Homo Sapien
US-10-176-482-598

```

Query Match	99.6%	Score 3699.5	DB 9	Length 705
Best Local Similarity	98.2%	Pred. No. 3.9e-295		
Matches 692	Conservative 0	Mismatches 0	Indels 13	Gaps 1
QY 1	MPVPWFLLSLALGRSPVVL	SLERLVGPQDATHCS	PGLSCLRWDSDIIL	CLPGDIVAPGPV 60
DB				
1	MPVPWFLLSLALGRSPVVL	SLERLVGPQDATHCS	PGLSCLRWDSDIIL	CLPGDIVAPGPV 60
QY 61	LAPTHLQTELVLRCQETDCD	LCRLRVAVHLAVHGWEEPEDEE	KFGGAADSGVVEEPNAS 120	
DB				
61	LAPTHLQTELVLRCQETDCD	LCRLRVAVHLAVHGWEEPEDEE	KFGGAADSGVVEEPNAS 120	
QY 121	LQAOVVLVSFOAYPTARC	VLELVQVPAALVQFGSGVSVYD	CFEALGSEVRIWSYTPQR 180	
DB				
121	LQAOVVLVSFOAYPTARC	VLELVQVPAALVQFGSGVSVYD	CFEALGSEVRIWSYTPQR 180	
QY 181	YEKELNHTQQLPALPML	NVSADGNVHLNVSEEQHGLSL	YWNQVGGPKPRWHKNLT 240	
DB				
181	YEKELNHTQQLPALPML	NVSADGNVHLNVSEEQHGLSL	YWNQVGGPKPRWHKNLT 240	
QY 241	GPQIITLNHTDLVPC	ICQWPLEPDSVRTNICPF	REDPRAHQLMWAARLLTL	LQSWL 300
DB				
241	GPQIITLNHTDLVPC	ICQWPLEPDSVRTNICPF	REDPRAHQLMWAARLLTL	LQSWL 300
QY 301	LDAPCSLPABAALCWR	APGDCQCPVPPISWENVVDK	VLEPPLKGHPNLQVQNSSE 360	
DB				
301	LDAPCSLPABAALCWR	APGDCQCPVPPISWENVVDK	VLEPPLKGHPNLQVQNSSE 360	
QY 361	KLOQLQCLWADSLGPK	LDVLLLETGCPQDNRSICAL	EPSCGCTSLPSKASTRAARL	GEYL 420
DB				
361	KLOQLQCLWADSLGPK	LDVLLLETGCPQDNRSICAL	EPSCGCTSLPSKASTRAARL	GEYL 420
QY 421	LQDLSGQCILQWLDD	DLGALWACPMQYIKHR	WALVWLACLLFAAALS	LTLCLKKHAK - 479
DB				
421	LQDLSGQCILQWLDD	DLGALWACPMQYIKHR	WALVWLACLLFAAALS	LTLCLKKHAKG 480
QY 480	-----	-----	-----	-----
DB				
481	WLRLLKQDVRSGAAR	GRAALLYSADDSGFERLV	GALASALCQLPLRVAV	DLWSRRELS 540
QY 528	AQCPVAWFHIAQRQTL	QEGGVVLLFSPGAVALC	SEWLQDVGSGCAHGH	PDHAFRSLSC 587
DB				
541	AQCPVAWFHIAQRQTL	QEGGVVVLLFSPGAVAL	CSEWLQDVGSGCAHGH	PDHAFRSLSC 600
QY 588	VLPDFLQGRAPGS	YVGACFDRLHLHPDAV	PALEFRTVPFTLPSQL	POFLGALQOPRAPRSG 647
DB				
601	VLPDFLQGRAPGS	YVGACFDRLHLHPDAV	PALEFRTVPFTLPSQL	POFLGALQOPRAPRSG 660
QY 648	RLOERAEOVS	RALQPALDSYFHP	PGTPAPGRGVGPGAG	PGAGDGT 692
DB				
661	RLOERAEOVS	RALQPALDSYFHP	PGTPAPGRGVGPGAG	PGAGDGT 705

Search completed: February 24, 2003, 09:25:00
Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 24, 2003, 09:20:41 ; Search time 47 Seconds
(without alignments)
1415.426 Million cell updates/sec

Title: US-09-608-918-2
Perfect score: 3716
Sequence: 1 MPVFWFLSLALGRSPVWLS.....TPAFGRGVGPGAGPGAGDCT 692

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	137.5	3.7	3707	2 S18252	heparan sulfate pr
2	130.5	3.5	1366	2 T35885	probable large prote
3	115.5	3.1	745	2 H85840	hypothetical prote
4	114.5	3.1	745	2 C99995	hypothetical prote
5	114.5	3.1	1193	2 F83264	hypothetical prote
6	113.5	3.1	761	2 S20458	hypothetical prote
7	111.5	3.0	478	2 D75564	pqqf protein - Kle
8	108	2.9	2629	2 T30987	hypothetical prote
9	107	2.9	719	2 T35189	telomerase-associa
10	107	2.9	825	1 A60386	probable ATP-depen
11	107	2.9	1118	1 A49724	interleukin-4 rece
12	104.5	2.8	238	2 C70841	protein-tyrosine-p
13	104.5	2.8	975	2 S33121	hypothetical prote
14	104.5	2.8	1711	1 A55148	homeotic protein C
15	104	2.8	1487	2 T02850	protein-tyrosine-p
16	103.5	2.8	676	1 WM8EX6	hypothetical prote
17	103.5	2.8	828	2 AD0412	ULF protein - huma
18	103.5	2.8	2055	2 T00093	ATP-dependent heli
19	103	2.8	8445	2 T31067	hypothetical prote
20	101.5	2.7	1151	2 S48431	BIR repeat contain
21	101	2.7	274	2 A73583	probable biotin sy
22	100.5	2.7	709	2 F75584	hypothetical prote
23	100.5	2.7	741	2 T31164	hypothetical prote
24	100.5	2.7	753	1 WZBEE8	gene 56 protein -
25	99	2.7	429	2 T36088	probable secreted
26	99	2.7	636	2 B83513	probable heat choc
27	99	2.7	660	2 E98169	serine proteinase
28	99	2.7	660	2 AB3118	conserved hypothet
29	99	2.7	679	2 B75262	

30	98.5	2.7	724	2 T47149	hypothetical prote
31	98.5	2.7	741	2 B49555	enhancer of split
32	98.5	2.7	1737	2 T02029	MEGF8 protein - hu
33	98	2.6	427	2 E87669	conserved hypothet
34	98	2.6	1487	1 EDDEE1	immediate-early pr
35	98	2.6	1487	1 EDDEF6	155K transcription
36	98	2.6	2205	1 MNWVRN	nonstructural poly
37	97.5	2.6	418	2 JC7588	exo-alpha-sialidas
38	97.5	2.6	617	2 F75484	hypothetical prote
39	97.5	2.6	698	2 A82593	hypothetical prote
40	97.5	2.6	850	2 JC5700	Erbb kinase activa
41	97.5	2.6	3739	2 T17410	polyketide synthas
42	97.5	2.6	4391	2 A38096	perlecan precursor
43	97	2.6	415	2 T46462	hypothetical prote
44	97	2.6	779	2 AG1978	hypothetical prote
45	97	2.6	2594	2 A35774	kinase-related pro

ALIGNMENTS

RESULT 1
S18252
heparan sulfate proteoglycan - mouse
N: Alternate names: perlecan
C: Species: Mus musculus (house mouse)
C: Date: 13-Jan-1995 #sequence, revision 13-Jan-1995 #text_change 05-Nov-1999
C: Accession: S18252; A31917; B31917; S66460
R: Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.;
J. Biol. Chem. 266, 22939-22947, 1991
A: Title: The complete sequence of perlecan, a basement membrane heparan sulfate prote
adhesion molecule.
A: Reference number: S18252; MUID: 92078153; PMID: 1744087
A: Accession: S18252
A: Molecule type: mRNA
A: Residues: 1-3707 <NO>
A: Cross-references: EMBL: M77174; NID: g200295; PIDN: AAA39911.1; PID: g200296
R: Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogell, G.; Sasaki, M.; Yamada, Y.; H
J. Biol. Chem. 263, 16379-16387, 1988
A: Title: Identification of cDNA clones encoding different domains of the basement mem
A: Reference number: A92680; MUID: 89034110; PMID: 2972708
A: Accession: A31917
A: Molecule type: mRNA
A: Residues: 940-1601 <NO2>
A: Cross-references: GB: J04054; NID: g200252; PIDN: AAA39899.1; PID: g200253
A: Accession: B31917
A: Molecule type: mRNA
A: Residues: 1870-2600 <NO3>
A: Cross-references: GB: J04055; NID: g200300; PIDN: AAA39912.1; PID: g200301
R: Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A: Title: Structural properties of recombinant domain III-3 of perlecan containing a g
A: Reference number: S66460; MUID: 95377282; PMID: 7649154
A: Accession: S66460
A: Molecule type: protein
A: Residues: 1272-1274, 'X', 1276, 'X', 1278-1279 <SCH>
C: Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G r
C: Keywords: glycoprotein
F: 199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F: 285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F: 325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F: 368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F: 764-811/Domain: laminin-type EGF-like homology <LEG>
F: 1159-1206/Domain: laminin-type EGF-like homology <LEG>
F: 1563-1610/Domain: laminin-type EGF-like homology <LEG>
F: 1613-1668/Domain: laminin-type EGF-like homology <EG7>
F: 3163-3198/Domain: EGF homology <EGF>
F: 3270-3423/Domain: laminin G repeat homology <LG2>
F: 3464-3492/Domain: EGF homology <EGF7>
F: 1256, 1891, 2336, 2394, 2427/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 3.7%; Score 137.5; DB 2; Length 3707;
Best Local Similarity 19.5%; Pred. No. 0.13;

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: H83640

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-745 <STO>

A:Cross-references: GB:AE005174; MID:g12516346; PIDN:AG57188.1; GSPDB:GN00145; UMGp:232

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

C:Gene: yehQ

C:Superfamily: *Escherichia coli* hypothetical 68.5K protein (molr-bglx region)

Query Match

Best Local Similarity 3.1%; Score 115.5; DB 2; Length 745;

Matches 162; Conservative 70; Mismatches 234; Indels 291; Gaps 43;

QY 21 LERLVGPQATH-----CSPGLSCLRLWSDILCLPGDIVPAPCPVLAPTHLOTFLVLR 74

DB 110 LEELATLPDTRKRAQVLVAKGITIELF-----CAPGEIPSARLP-MSDVRFSRSIRF 163

QY 75 QKETDC---DLCRLVAVHLAVHGHWEPEDEEKF-----GGAADSGVEEPRNA 119

DB 164 AR-CDCIETGLCEHV--LAVQAFVEAKTQAEETHLIWQMRSEHVTSSDDPFASEGNA 220

QY 120 SLQ-----AQVLSFOA-----YPTARCVLLEVOVPAALVQFGOSVGV 159

DB 221 CRQYVQQLSOALWLGISQPLIHYEAFSAQQAERCNWR--WVSESLRQLRASV--- 274

QY 160 YDCFEAA-----LGSEVRINWSTQPRYKELNHTQOL-----PALPWLNVSDG-- 203

DB 275 -DAFHARASHYHAGECLRLQALNSR-----LNCQAEMARRDSVGEVPPVPMRTVVGSGIA 329

QY 204 -----DNVHLV-LNV---SEQHFGLSLVWNOVGQPKPRWKNLTGPIITLNHTDLPV 254

DB 330 GEAKLDHLRLVSLGRCWQDIEHYGLRIWF-----TDPDGTSLILHS--- 371

QY 255 CLCIQVWPLEPDSVRTNICPFREDPRAHONLWQAARLLTLQSWLL-----DAPCS 306

DB 372 -----RSPRSEQENSPAATRRLSFQAGALAGQIVSOAAKRS 410

QY 307 LPAEAALCWRAFGDPCQPLVP--PLSWENVTVDKLEFPL-----LKGHPNLC 353

DB 411 ADGELLATR-----NRLSSVVPPLSPDAW-----RMLSAPLRQPGIVALREYLQRPPSC 460

QY 354 V-----QVNSSEKIQLOECL--WADSLGPKDDVLLLETRGPQDNRSICALPSCGCTSLP 406

DB 461 IRPLNQVDNLFILPVAECISLGDSSRQTL--DAQVISGEG-EDN--LLTL-----SLP 509

QY 407 SKASTRAA--RLGEYLLDQSGQCL-----QLWDDD----- 436

DB 510 ASASAPYAVERMAA--LLQOTDDPVCVLSGVFSVDGQLTLEPQVMMTKTRAWALDAETAP 568

QY 437 ----LALWACPMCKYIHKRWALVWLACLLFAAALSILLLKKD--HAKAAARGRAALLL 490

DB 569 VVASLPSASVLPVPSAHQ-----LLMRCQALLQLLHNGWRYEQSAIGQAEALLA 619

QY 491 YSADDSGFERLVGALASALCOLPLRVAVDLWSRRSLSAQGPVAFWFAQRQTLOEGGVV 550

DB 620 NDLTAVGFYRLAHVL-----GQFRNTESEARVEA 648

QY 551 LLFSPGAVALCSEWL-----QDGVSGPGANG-----PHDAFR---ASLSCVLPDFLQ 594

DB 649 M---NNGVLLCEQLFPLQOQGLNRPFGCEFCICELRLPDHRFRWKNKFLFLLP--- 702

QY 595 GRAPGSYVGCDFRLHPDAVPALFTVPVFTLPSOL 631

DB 703 -----EHGPAFAI---VDCYTSPTPL 721

RESULT 4

C99995

hypothetical protein Ecs2931 [Imported] - *Escherichia coli* (strain O157:H7, substrain R)

C:Species: *Escherichia coli*

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002

C:Accession: C99995

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and g

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: C99995

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-745 <RAY>

A:Cross-references: GB:BA000007; PIDN:BA36354.1; PID:g13362400; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RMD 0509952

C:Genetics:

C:Gene: Ecs2931

C:Superfamily: *Escherichia coli* hypothetical 68.5K protein (molr-bglx region)

Query Match

Best Local Similarity 3.1%; Score 114.5; DB 2; Length 745;

Matches 163; Conservative 69; Mismatches 236; Indels 287; Gaps 43;

QY 21 LERLVGPQATH-----CSPGLSCLRLWSDILCLPGDIVPAPCPVLAPTHLOTFLVLR 74

DB 110 LEELATLPDTRKRAQVLVAKGITIELF-----CAPGEIPSARLP-MSDVRFSRSIRF 163

QY 75 QKETDC---DLCRLVAVHLAVHGHWEPEDEEKF-----GGAADSGVEEPRNA 119

DB 164 AR-CDCIETGLCEHV--LAVQAFVEAKTQAEETHLIWQMRSEHVTSSDDPFASEGNA 220

QY 120 SLQ-----AQVLSFOA-----YPTARCVLLEVOVPAALVQFGOSVGV 159

DB 221 CRQYVQQLSOALWLGISQPLIHYEAFSAQQAERCNWR--WVSESLRQLRASV--- 274

QY 160 YDCFEAA-----LGSEVRINWSTQPRYKELNHTQOL-----PALPWLNVSDG-- 203

DB 275 -DAFHARASHYHAGECLRLQALNSR-----LNCQAEMARRDSVGEVPPVPMRTVVGSGIA 329

QY 204 -----DNVHLV-LNV---SEQHFGLSLVWNOVGQPKPRWKNLTGPIITLNHTDLPV 254

DB 330 GEAKLDHLRLVSLGRCWQDIEHYGLRIWF-----TDPDGTSLILHS--- 371

QY 255 CLCIQVWPLEPDSVRTNICPFREDPRAHONLWQAARLLTLQSWLL-----DAPCS 306

DB 372 -----RSPRSEQENSPAATRRLSFQAGALAGQIVSOAAKRS 410

QY 307 LPAEAALCWRAFGDPCQPLVP--PLSWENVTVDKLEFPL-----LKGHPNLC 353

DB 411 ADGELLATR-----NRLSSVVPPLSPDAW-----RMLSAPLRQPGIVALREYLQRPPSC 460

QY 354 V-----QVNSSEKIQLOECL--WADSLGPKDDVLLLETRGPQDNRSICALPSCGCTSLP 406

DB 461 IRPLNQVDNLFILPVAECISLGDSSRQTL--DAQVISGEG-EDN--LLTL-----SLP 509

QY 407 SKASTRAA--RLGEYLLDQSGQCL-----QLWDDD----- 436

DB 510 ASASAPYAVERMAA--LLQOTDDPVCVLSGVFSVDGQLTLEPQVMMTKTRAWALDAETAP 568

QY 437 ----LALWACPMCKYIHKRWALVWLACLLFAAALSILLLKKD--HAKAAARGRAALLL 490

DB 569 VVASLPSASVLPVPSAHQ-----LLMRCQALLQLLHNGWRYEQSAIGQAEALLA 619

QY 491 YSADDSGFERLVGALASALCOLPLRVAVDLWSRRSLSAQGPVAFWFAQRQTLOEGGVV 550

DB 620 NDLTAVGFYRLAHVL-----GQFRNTESEARVEA 648

QY 551 LLFSPGAVALCSEWL-----QDGVSGPGANGPHDAFRASLSCVLPD-----FLOGR 596

DB 649 M---NNGVLLCEQLFPLQOQGLNRPFG--PGECEICELR--LPDHRFRWKNKFLF--- 698

QY 597 APGSYVGCDFRLHPDAVPALFTVPVFTLPSOL 631

DB 699 -----LLPEEYGPAPFAIIVDCYTSPTPL 721

RESULT 5
F83264
hypothetical protein PA3063 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83264
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bladen, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, N.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: F83264
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1193 <STO>
A:Cross-references: GB:AE004730; GB:AE004091; NID:g9949154; PIDN:AAG06451.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3063

Query Match 3.1%; Score 114.5; DB 2; Length 1193;
Best Local Similarity 21.7%; Pred. No. 1.8;
Matches 154; Conservative 53; Mismatches 240; Indels 263; Gaps 38;
QY 81 DCLRVAVHLVGHWE-----EPDEKEFGGAADSGV---EPRNASLQAQVY--- 126
DB 293 DLRLNNAAG-RVERAWEVQCELLALRPEDRTLLADLARLGWTGNGPRALGFWKQLLAGA 351
QY 127 -----LSFOAYPTARCVLLEVPVPAALVQFGSQSVGVYDCFEAALGSEVRW- 174
DB 352 DDPALREHAWRLSQMFDFDSALIELLAPCAQOMTDELDALVYSHETRGTPPEGAWL 411
QY 175 -SYTOPREKE-----LNHTQOLPALP--WLVNSADGDNVHLNVSEEQHFGLS 221
DB 412 RGYVQ-RYPKQRLAWQRLQILEHTQOLQEBETGVWARMAR-----HFPLSVKRMQWA-E 464
QY 222 LYNNVQGGPKPRWHKNTLGPQIITLNTHTDLVPCICIQWPLEPD-----SV 268
DB 465 THWNLFD--PROAW-KVLAVGVDTAIREPEFWRLRAALAWALEODDDARAAYERMALDI 521
QY 269 RTN-----ICPFRED--PRAHQNL--WOAAR-----LRLLTQSWLLDAPC--SLPA 309
DB 522 RLNSRDEDLTALYRDSNPQALQVLIGSWQSRDRPRLASALQLAENLHDWPAKLSLLA 581
QY 310 BAALCWAPGGDPCQPLVPLSW-----ENVTVKVLFFPLKKGHPNLC 353
DB 582 EAEGLEPAQGS-----PYWVARARLAEQHGCDVAERLYREALVREP----- 624
QY 354 VQVNSSEKLOQECWL-----ADSLGP-----LKDDV-----LLLETRGP 388
DB 625 -----GENLVRERLLWFYIDGRRDSLAPLLAQWHLALRDLSTLMLPFASASLLE- 675
QY 389 QDNRLSC-----ALEPSGCTSLPSKASTRAARLGEVLLQDLQSG 427
DB 676 RNDQALAWFRLLYLSNPNDLVQAAYADLDSG-----YQDKALRLRLRLRL- 725
QY 428 QCLQLWDDDLGALWACPMKDYIHKRWLVWLACLLFFAAALSLL-LLKKDHAKAAA 482
DB 726 -----DREAVRATPDS-----FATYLRLLAVAQGPPLAQGEARRAW 761
QY 483 RGRAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELSAQGPVAMFHAQRROT 542
DB 762 NGEPAML-----QLWFEQFLDQLA-ATNOEPLK-----DNW-----LAWARGRLKI 802
QY 543 LOEGGVVVVLLFSPCAVALCSEWLQDVGSGPG-----AHGPHDAFRASUSCVLPDFL 593
DB 803 GRNEIQAAALRSQNAAL-QRLRGELGDLPAQRVEALVRLGHG----- 844
QY 594 QGRAPGSYVGACFD-----RLHPDPAVPAFLFTVPVFTLPSQLPDRFG 636

DB 845 -GEALGALGALGDGHSRDNREQLRRAQAAILERTTQGLQLGNKRDFFG 893

RESULT 6
S20458
pqgF protein - Klebsiella pneumoniae
C:Species: Klebsiella pneumoniae
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 24-Sep-1999
C:Accession: S20458
R:Meulenbergh, J.J.M.; Sellink, E.; Riegman, N.H.; Postma, P.W.
Mol. Gen. Genet. 232, 284-294, 1992
A:Title: Nucleotide sequence and structure of the Klebsiella pneumoniae pqg operon.
A:Reference number: S20452; MUID:92212293; PMID:1313537
A:Accession: S20458
A:Molecule type: DNA
A:Residues: 1-761 <MEU>
A:Cross-references: EMBL:X58778; NID:g43903; PIDN:CAA41584.1; PID:g43909
C:Genetics:
A:Gene: pqgF
C:Superfamily: pyrroloquinoline quinone synthesis F protein

Query Match 3.1%; Score 113.5; DB 2; Length 761;
Best Local Similarity 23.4%; Pred. No. 1.2;
Matches 117; Conservative 50; Mismatches 165; Indels 167; Gaps 27;
QY 282 HQNLWQAARLRLTLTQSWLLDAPCSLPAPALCWAPGG---DPCQPLVPPLSWENVTVD 338
DB 182 HRTYVAVARMQL-----W-LOGPOSLEALGELAARFAAGLAAGEAPPAPPL- 227
QY 339 KVLPEPLKLGHPNLCVQVNSSEKLOECLWADSLGPKDDVLLLTGRGPQDNRSICAL 398
DB 228 RLGETALQ-----LAVSS-----QPALWRCPLTALSNDVTLR- 261
QY 399 PSGTSLPSKASTRAARLGEYLQD-----LQSGQCQLQWLWDDDLGALWACPMKDYIHKRW 454
DB 262 -----EFLDEAPGSLMAGLRQRRLAGDVALNW-----LYQDRH 295
QY 455 LWVLAACLLFAA-----ALSLILLKKDHAKAAARGRAALL----- 489
DB 296 LGWLA-LVFASDRPEVDVDRQIHWLQALQQTTPQQQHYQLSRRRFFQALSPDLQRLORA 354
QY 490 ---LYSADDSGFERLVGAL-----ASALCQ-----LPLRVAVDLWSRRELS 527
DB 355 FGFAAGPAPGAFDFCAALQVAPSVSLACQTVSPGEPVATGFSLPL-----SRWRRRPES 410
QY 528 AQGPVAMFHAQRROT-----QEGGVVVLLFSPG-----AVALCSEWLQDGVY- 570
DB 411 DPALAFAYFOAAGDLVAKCEKAPLHLPSGDPPLRLRPFPYCSPDQAEGLARGEQ 470
QY 571 -----GFGAHGPHDAFRAS--LSCVLPDFLQGRAPGSYVAGACFDRLLHPDA--VPA 617
DB 471 LRPLAALRHAGGHEWHLFDGSMQTLQLPE--PGRPEAILQAILQLALPVASLTPS 528
QY 618 LFRVTVFTLPSQLPDFLIGALQQR-----APRSGRLQERAEQVSRALQALPDYSYFHPGTP 674
DB 529 P-ESIALRHMAQLPERLGTSGHQKWLALAGGSAEDAQWVAROLS-LITAPVNP-MP 585
QY 675 APG---RGVGGAGPGAGD 690
DB 586 APAPCRGVRVERLYVPG-GD 603

RESULT 7
D75564
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: D75564
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.


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QY 449 IHKRWLVWLAACLLFAALSL-----ILLKKHAKAAAGRAALLLYSADDS 496
      |||
Db 440 -----AWVARQAEQAAREYVSTRCRMEFLQRLDDEKAAPCGRCDCAGPWLDP 492
      |||
QY 497 GFERLVGALASALCOLPLRVAVDLWSR-----ELSAQGPVAFWHAQRRTLOE 545
      |||
Db 493 AVS--AGALAAATGELD-RGVVEPRKMTPTGLAAVGMCLKGRIPAG-----RQAL-T 542
      |||
QY 546 GGVVLLFSPGAVALCSEW---LQDGVSGPGAHC--PHDAFRASLSCLVLPDFLOGRAPS 600
      |||
Db 543 GRALGRLSDIG-----WGNRLRPLLSAQAAGVPDDVLRAVVT-VLADW--ARSPGG 592
      |||
QY 601 YGACEDRLLLHPDAVPALFTVPVFTLPSQL-PDFLGAQQAPRAPRSGRQLQERAEQVSRA 659
      |||
Db 593 WATG-----SPDAVA---RPVGWVAVPSRTRPOLVGSIAEVA-RVGR-----632
      |||
QY 660 LQALDSYFHP 671
      |||
Db 633 ---PLLGSLAHTP 642

RESULT 10
A:60386
Interleukin-4 receptor precursor - human
N:Alternate names: IL-4 receptor
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A60386; A47603
R:Galizzi, J.P.; Zuber, C.E.; Harada, N.; Gorman, D.M.; Djossou, O.; Kastelein, R.; Banc
Int. Immunol. 2, 669-675, 1990
A:Title: Molecular cloning of a cDNA encoding the human interleukin 4 receptor.
A:Reference number: A60386; MUID:91120547; PMID:2278997
A:Accession: A60386
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-825 <GAL>
R:Idzerda, R.L.; March, C.J.; Mosley, B.; Lyman, S.D.; Vanden Bos, T.; Gimpel, S.D.; Di
J. Exp. Med. 171, 861-873, 1990
A:Title: Human interleukin 4 receptor confers biological responsiveness and defines a n
A:Reference number: A47603; MUID:90171849; PMID:2307934
A:Accession: A47603
A:Molecule type: mRNA
A:Residues: 1-74, 'I', 76-825 <IDZ>
A:Cross-references: GB:X52425; NID:g33833; PIDN:CAA36672.1; PID:g33834
C:Genetics:
A:Gene: GDB:IL4R
A:Cross-references: GDB:118823; OMIM:147781
A:Map position: 16p12.1-16p12.1
C:Superfamily: Interleukin-4 receptor; cytokine receptor homology
C:Keywords: cytokine receptor; glycoprotein; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-825/Product: interleukin-4 receptor #status predicted <MAT>
F:26-232/Domain: extracellular #status predicted <EXT>
F:34-218/Domain: cytokine receptor homology <CRS>
F:233-256/Domain: transmembrane #status predicted <TMW>
F:257-825/Domain: intracellular #status predicted <INT>
F:53, 98, 128, 134, 176, 209/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.9%; Score 107; DB 1; Length 825;
Best Local Similarity 19.2%; Pred. No. 4.3;
Matches 155; Conservative 66; Mismatches 284; Indels 304; Gaps 36;

QY 41 LWSDSILCPGDIVP-----AGPVLVAPHLOTELVLRCQKETDCDLCRLVAVHLAVH 93
      |||
Db 103 LWAGQQLLWKGSKPSEHKVPKRAPGNLVHTNVSDTLTLTWSNPYPDPDNLNHLTYAVN 162
      |||
QY 94 GHWPEDEEERFGGAADSGVEEPRNASLQAQVLSFQAYPTARCILLE--VQVPALVQF 151
      |||
Db 163 -IWSENDPAD-----FRYI---NVTYLEPSLRIAASTLS 193
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QY 152 QGVSQSVVYDCFEAALGSEVRIWSYTOPRYEKELNHTQOLPALPWNVSADGDNVHLVNL 211
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Db 194 GIS-----YRARVRAWAOCY-----NTTWSESPSTKWHNSYREPEQHLILG 236
QY 212 VSEEQHGLSL-----YWNQVQGPCKPR-----WHKNLTGPQI 244
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Db 237 VSVSCIVILAVCLLCVYSTIKKEMWDQIPNPARSLVAIIITQDAQSOWEKSRGQEP 296
      |||
QY 245 ITLNH-----TDLVPCCLCIVVWPLEPDSVRTNICPREDPRAHQNLOWARLRLTLQSW 299
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Db 297 AKCPHWKNCILTKLLFCF-----LEHMKRD-----EDPH-----KAA--KEMPFQGS 336
      |||
QY 300 LIDAPCSLPAEALCWRAFPGDPCQPLVPPLSWENVTVDKVLEFPL-----LKGH 349
      |||
Db 337 GKSACWCPVEISKTVLW-----PESISVVCVELPEAPVECEEEVEEKEG-- 382
      |||
QY 350 PNLQVQVNSSEK-----LQLOECLWADSLGPKDKDVLLETRG---PDNRSLCA 396
      |||
Db 383 -SFCASPESSRRDFOEGREGIVARLTESLFLDLG-----EBGGFCQDDMGESCL 432
      |||
QY 397 LEPSGCTS-----LPSKASTRAARLGYLLQDLSQGQCLOLWDDDLGALWACPMKYI 449
      |||
Db 433 LPPSGSTSAHMPWDEFFSAGPKAPPGWK-----EQPLHLEPSPAPSTQSPDN--- 481
      |||
QY 450 HKRWLVWLAACLLFAAALSILLKKHAKAAAGRAALLLYSADDSGPERLVGALASAL 509
      |||
Db 482 -----LTC-----TETPLVIAGNPATRSFNSLSQSP 508
      |||
QY 510 COLPLRVAVDLWSRRELS-----AQGPVAFWHAQRRTLOEGGVVV 550
      |||
Db 509 C--PRELGPDPLLARHLHEVEPEMPCVQLSEPTTVQPEPETWEQILRRNVLQHCAAAA 566
      |||
QY 551 LLFSP--CAVALCSEWLQDGV-----GPAHGPDAFRASL--SCVLPDFLO-GRAP 598
      |||
Db 567 PVSAPTSQYQEFVHAVEQGTQASAVVGLGPGGEAGYKAFSLLASSAVSPEKCGFGASS 626
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QY 599 GSYVGACFDRL-----HPDAVPALFTVPVFT-----LPSQLPDLFGA- 637
      |||
Db 627 GEEGKFPQDILPCGPGDPAPVP-----VPLFTFGLDREPRSPSSHLPSSSPHEHGLE 681
      |||
QY 638 -----LQOPRAPRS-----GRLOERAQVSRALQPALDS 666
      |||
Db 682 PGEKVEDMPKPLPQEQATDPLVDSLSGIVYSALTCHLCHLKOCHQEDGGGQTPVMAS 741
      |||
QY 667 -----YFHPGCTPAPGRGVGPGAGP 686
      |||
Db 742 PCGCCGCCGDRSSPTTTLRAPDPSPGVP 770

RESULT 11
A:49724
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type H precursor - human
N:Alternate names: protein-tyrosine-phosphatase, stomach cancer-associated type 1; SA
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 23-Feb-1996 #text_change 16-Jun-2000
C:Accession: A49724
R:Watozaki, T.; Suzuki, T.; Uchida, T.; Inazawa, J.; Ariyama, T.; Matsuda, K.; Horita
J. Biol. Chem. 269, 2075-2081, 1994
A:Title: Molecular cloning of a human transmembrane-type protein tyrosine phosphatase
A:Reference number: A49724; MUID:94124561; PMID:8294459
A:Accession: A49724
A:Molecule type: mRNA
A:Residues: 1-1118 <MAT>
A:Cross-references: GB:D15049; NID:g475003; PIDN:BAA03645.1; PID:g475004
C:Genetics:
A:Gene: GDB:PTPRH; SAP-1
A:Cross-references: GDB:305504
A:Map position: 19q13.4-19q13.4
A:Note: highly expressed in colon and pancreatic cancer cells but not in the normal c
C:Superfamily: protein-tyrosine-phosphatase, receptor type H; fibronectin type III re
C:Keywords: carcinogenesis; duplication; glycoprotein; phosphoprotein; phosphoric mon
F:1-27/Domain: signal sequence #status predicted <SIG>
F:27-110/Domain: fibronectin type III repeat homology <3FNA>
F:28-1118/Product: protein-tyrosine-phosphatase, receptor type H #status predicted <M
F:28-761/Domain: extracellular #status predicted <EXT>
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F:116-199/Domain: fibronectin type III repeat homology <3FNB>
F:205-289/Domain: fibronectin type III repeat homology <3FNC>
F:296-379/Domain: fibronectin type III repeat homology <3FND>
F:385-468/Domain: fibronectin type III repeat homology <3FNE>
F:474-558/Domain: fibronectin type III repeat homology <3FNF>
F:564-658/Domain: fibronectin type III repeat homology <3FNG>
F:667-737/Domain: fibronectin type III repeat homology <3FNH>
F:762-778/Domain: transmembrane #status predicted <TMN>
F:779-1118/Domain: intracellular #status predicted <INT>
F:846-1070/Domain: protein-tyrosine-phosphatase homology <PTPI>
F:35,78,83,107,132,149,172,196,203,286,304,312,329,352,376,383,401,436,439,470,490,558,578,600,627,654,681,708,735,762,789,816,843,870,897,924,951,978,1005,1032,1059,1086,1113,1140,1167,1194,1221,1248,1275,1302,1329,1356,1383,1410,1437,1464,1491,1518,1545,1572,1599,1626,1653,1680,1707,1734,1761,1788,1815,1842,1869,1896,1923,1950,1977,2004,2031,2058,2085,2112,2139,2166,2193,2220,2247,2274,2301,2328,2355,2382,2409,2436,2463,2490,2517,2544,2571,2598,2625,2652,2679,2706,2733,2760,2787,2814,2841,2868,2895,2922,2949,2976,3003,3030,3057,3084,3111,3138,3165,3192,3219,3246,3273,3300,3327,3354,3381,3408,3435,3462,3489,3516,3543,3570,3597,3624,3651,3678,3705,3732,3759,3786,3813,3840,3867,3894,3921,3948,3975,4002,4029,4056,4083,4110,4137,4164,4191,4218,4245,4272,4299,4326,4353,4380,4407,4434,4461,4488,4515,4542,4569,4596,4623,4650,4677,4704,4731,4758,4785,4812,4839,4866,4893,4920,4947,4974,5001,5028,5055,5082,5109,5136,5163,5190,5217,5244,5271,5298,5325,5352,5379,5406,5433,5460,5487,5514,5541,5568,5595,5622,5649,5676,5703,5730,5757,5784,5811,5838,5865,5892,5919,5946,5973,6000,6027,6054,6081,6108,6135,6162,6189,6216,6243,6270,6297,6324,6351,6378,6405,6432,6459,6486,6513,6540,6567,6594,6621,6648,6675,6702,6729,6756,6783,6810,6837,6864,6891,6918,6945,6972,6999,7026,7053,7080,7107,7134,7161,7188,7215,7242,7269,7296,7323,7350,7377,7404,7431,7458,7485,7512,7539,7566,7593,7620,7647,7674,7701,7728,7755,7782,7809,7836,7863,7890,7917,7944,7971,7998,8025,8052,8079,8106,8133,8160,8187,8214,8241,8268,8295,8322,8349,8376,8403,8430,8457,8484,8511,8538,8565,8592,8619,8646,8673,8700,8727,8754,8781,8808,8835,8862,8889,8916,8943,8970,8997,9024,9051,9078,9105,9132,9159,9186,9213,9240,9267,9294,9321,9348,9375,9402,9429,9456,9483,9510,9537,9564,9591,9618,9645,9672,9699,9726,9753,9780,9807,9834,9861,9888,9915,9942,9969,10000,10001,10002,10003,10004,10005,10006,10007,10008,10009,10010,10011,10012,10013,10014,10015,10016,10017,10018,10019,10020,10021,10022,10023,10024,10025,10026,10027,10028,10029,10030,10031,10032,10033,10034,10035,10036,10037,10038,10039,10040,10041,10042,10043,10044,10045,10046,10047,10048,10049,10050,10051,10052,10053,10054,10055,10056,10057,10058,10059,10060,10061,10062,10063,10064,10065,10066,10067,10068,10069,10070,10071,10072,10073,10074,10075,10076,10077,10078,10079,10080,10081,10082,10083,10084,10085,10086,10087,10088,10089,10090,10091,10092,10093,10094,10095,10096,10097,10098,10099,10100,10101,10102,10103,10104,10105,10106,10107,10108,10109,10110,10111,10112,10113,10114,10115,10116,10117,10118,10119,10120,10121,10122,10123,10124,10125,10126,10127,10128,10129,10130,10131,10132,10133,10134,10135,10136,10137,10138,10139,10140,10141,10142,10143,10144,10145,10146,10147,10148,10149,10150,10151,10152,10153,10154,10155,10156,10157,10158,10159,10160,10161,10162,10163,10164,10165,10166,10167,10168,10169,10170,10171,10172,10173,10174,10175,10176,10177,10178,10179,10180,10181,10182,10183,10184,10185,10186,10187,10188,10189,10190,10191,10192,10193,10194,10195,10196,10197,10198,10199,10200,10201,10202,10203,10204,10205,10206,10207,10208,10209,10210,10211,10212,10213,10214,10215,10216,10217,10218,10219,10220,10221,10222,10223,10224,10225,10226,10227,10228,10229,10230,10231,10232,10233,10234,10235,10236,10237,10238,10239,10240,10241,10242,10243,10244,10245,10246,10247,10248,10249,10250,10251,10252,10253,10254,10255,10256,10257,10258,10259,10260,10261,10262,10263,10264,10265,10266,10267,10268,10269,10270,10271,10272,10273,10274,10275,10276,10277,10278,10279,10280,10281,10282,10283,10284,10285,10286,10287,10288,10289,10290,10291,10292,10293,10294,10295,10296,10297,10298,10299,10300,10301,10302,10303,10304,10305,10306,10307,10308,10309,10310,10311,10312,10313,10314,10315,10316,10317,10318,10319,10320,10321,10322,10323,10324,10325,10326,10327,10328,10329,10330,10331,10332,10333,10334,10335,10336,10337,10338,10339,10340,10341,10342,10343,10344,10345,10346,10347,10348,10349,10350,10351,10352,10353,10354,10355,10356,10357,10358,10359,10360,10361,10362,10363,10364,10365,10366,10367,10368,10369,10370,10371,10372,10373,10374,10375,10376,10377,10378,10379,10380,10381,10382,10383,10384,10385,10386,10387,10388,10389,10390,10391,10392,10393,10394,10395,10396,10397,10398,10399,10400,10401,10402,10403,10404,10405,10406,10407,10408,10409,10410,10411,10412,10413,10414,10415,10416,10417,10418,10419,10420,10421,10422,10423,10424,10425,10426,10427,10428,10429,10430,10431,10432,10433,10434,10435,10436,10437,10438,10439,10440,10441,10442,10443,10444,10445,10446,10447,10448,10449,10450,10451,10452,10453,10454,10455,10456,10457,10458,10459,10460,10461,10462,10463,10464,10465,10466,10467,10468,10469,10470,10471,10472,10473,10474,10475,10476,10477,10478,10479,10480,10481,10482,10483,10484,10485,10486,10487,10488,10489,10490,10491,10492,10493,10494,10495,10496,10497,10498,10499,10500,10501,10502,10503,10504,10505,10506,10507,10508,10509,10510,10511,10512,10513,10514,10515,10516,10517,10518,10519,10520,10521,10522,10523,10524,10525,10526,10527,10528,10529,1053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Db 469 VTSLOPQOGCVSSSESTPKTSASCPAPSPSSSVKSLT---ELVQPCP-PIET- 523
QY 313 LCWRAPGGDCQPLVPPLSWENVTVDKLEFPL-LKGHPNLCVQ--VNSSSEKL----- 362
Db 524 ----SKDKRPFESDPAS-----DSQATPLPLSGHSALSIQELVAMSPELDTYGITK 573
QY 363 QLOECLWADSLG-LKDDVLLLETRG-----PDNRSCLALPPSGCTSLPSKAST 411
Db 574 RVKEVLTNNIGQLRFGETILGLTGQSVSDLLSRPKPWHKLSLKGREFP----- 622
QY 412 RAARLGEYLLQDLSQGCLOLWDDDDGALWACPMKDYIHKRWALVWLAACLLFAAALSIL 471
Db 623 ----VRMQLWLD-----PNN-----VEKLM 639
QY 472 LLKKDHAKAARGRAALLYSADDS-----GFERLVG----- 503
Db 640 DMKMEKKAYMKRRHS-----SVSDSQCEPPSPGIDYSOGASPOQHOLKKPRVYLAPEE 695
QY 504 --ALASALCQLPL---RVAVDLWSRRELSAQGPVAMFHAQRROTLOEGGVVVLFLSPGAV 558
Db 696 KEALKRAYOQKPPSPKTIIEELATQLNLTSTVINWFHNYRSRIRRE----- 742
QY 559 ALCSEWLQGVSG-PGA-HGPHDAFRASLSCVLPDLFQGRAPGSYVGAC--FDRLLHPDA 614
Db 743 -LFIEIOAGSOGQAGARHSP--SARSS-----GAAPSSEGSDCDGEAAEGPGA 789
QY 615 VPALFRTVPVFTLPOLDFLQALQOPRPRSGRLQERAEQVSRALQALPDSFHPHGT- 673
Db 790 ADA-EESAPAAAKSO-----GGPAEAAVAP-----EERE-----APRAEKRSRRPRGPG 835
QY 674 PAPGRGVGPGAGPGA 688
Db 836 PGPGRRGGGPGAPGA 850

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RESULT 14

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A55148
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type OST precursor - rat
N:Alternate names: OST-PPP; osteotesticular protein-tyrosine-phosphatase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R:Mauro, L.J.; Olmsted, E.A.; Skrobacz, B.M.; Mourey, R.J.; Davis, A.R.; Dixon, J.E.
J. Biol. Chem. 269, 30659-30667, 1994
A:Title: Identification of a hormonally regulated protein tyrosine phosphatase associated
A:Reference number: A55148; MUID:95074080; PMID:7527035
A:Accession: A55148
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1711 <MAU>
A:Cross-references: GB:L36884
C:Comment: The sequence contains ten fibronectin type III repeats and two protein-tyrosin
C:Superfamily: protein-tyrosine-phosphatase, receptor type OST; fibronectin type III rep
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane pro
F:1-18/Domain: signal sequence #status predicted <STG>
F:19-1711/Product: protein-tyrosine-phosphatase, receptor type OST #status predicted <MA
F:1174-1398/Domain: protein-tyrosine-phosphatase homology <PTPI>
F:1350/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1356/Binding site: substrate phosphate (Arg) #status predicted

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Query Match 2.8%; Score 104.5; DB 1; Length 1711;
Best Local Similarity 18.8%; Pred. No. 17;
Matches 150; Conservative 80; Mismatches 274; Indels 293; Gaps 37;
QY 5 WFLLSLALG-RSPVVLSERLVGPQDATHCSPLGSLRWLSDILCLPGDIVPAPGPVLAP 63
Db 322 WASNKAGLGARDGYVL---KLSGPMESTSLGPECN-----AVFPGP-LPP 364
QY 64 THLQTELVRCKQETDCDLCLRVAVHLAVHGWHEPDEBEKFGGADSGVEE----PRNA 119
Db 365 GHYTLQL-----KVLGAPVDANVEGSTWLAESEA 392

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QY 120 SLQAQVW-----LSFOAYPTARCVLLEVQVPAALVOFGQSVGS--VYVDCEAALGS 169
Db 393 ALPREVPGARLWDGLEASKQGRRALLYSDDAPGSLGNISVPSGATHVIFCGLVGAHY 452
QY 170 EVRIWSTQPRYEKELNHTQQLP--ALPWLNVNSADGDNVHLNVSEEQHFGLSLXNQV 227
Db 453 RVDIASSTGDISQSISGYTSPLPQPSLEVISRSPSD-----LTIANGPA 497
QY 228 QGP---PRPRWIKNLT-----GPOITLNLHTDLP--CLCIQVNP-----LEPDSV 268
Db 498 PQOLEGYKVYTHQDGSQSRSPGDLVDLGPDTLSLTLSKSLVPGSSYTVSAWAGNLSGDSQ 557
QY 269 RTNIPC-----FREDPRAHONLW-----QAARLRLTLQ----- 297
Db 558 KIHSTRAPPTNLSLGFPAHQFAALKASWYHPPGGRDFAHLRLYLRLPLTLESEKVLPRE 617
QY 298 ----SWL-LDAPCSLPAEAAALCW-----RAPGDDPCQPLVPPLSWENVTVDKVLFP 344
Db 618 AQNFSQAOLTAGCEQVQLSTLWGSERSSSANATGTP--PSAPTL--VNVTSDAFTQLQ 673
QY 345 LLKHPNLCVQVNSSEKIQLOECLMADS-----LGPLKDDVLLLETRGPQDNRSICAL 397
Db 674 VSWAHV-----PGGRSRYQVTLYOESTRTATSIIMP-----KEDGTSFLGL 714
QY 398 EPS-----GCTSLPSKASTRAARLGEY-----LLQDLSQGCLOLWDDDLGALWACP 444
Db 715 TPGTKYKVEVISWAGPLYTAAANSAWYPLIPNELLVSMOAGSAVV----- 761
QY 445 MDKYHKRWALVWLAACLLFAAALSILLKDKHAKAARGRAALLYSADDSGFERLVGA 504
Db 762 ----NLAWPSGLQGGAC-----HAOLSDAGHLS----- 786
QY 505 LASALCQLPLRVAVDLWSRRELSAQGPVAMFHAQRROTLEQ-GVVVLLFSPGAVALCSE 563
Db 787 ----WEQPLKLGQELFMRDLTTPGHTTISMSVRCRAGPLQAATHLVLSVEGPV---- 836
QY 564 WLQGVSGFGAGHPDAFRASLSCVLPD-----FQGRAPGS-----YVGACFDR 609
Db 837 --EDVLCHP-----EATYLAALNWTMPAGDVDCVLVWVERLVPGGGTHFVFOVNTSGDAL 888
QY 610 LHPDAVPALFRTVPVFTLPOLDFLQALQOPRPRSGRLQERAEQVSRALQALPDSYFH 669
Db 889 LLPNLMTPTSYRLSLTVL-----GRNSRWSRAVSLVCS TSAEW-H 928
QY 670 PPGTPAP-----GRGVG 681
Db 929 PPELAEPPOVELGTGMG 945

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RESULT 15

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T02850
hypothetical protein L1439.2 [imported] - Leishmania major (strain Friedlin)
C:Species: Leishmania major
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
C:Accession: F81462; T02850
R:Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protei
A:Reference number: A81455; MUID:99178987; PMID:10077609
A:Accession: F81462
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1487 <PYL>
A:Cross-references: GB:AE001274; NID:g3264850; PIDN:ACC24673.1; PID:g2266918; GSPDB:G
A:Experimental source: strain WHOM/IL/81/Friedlin
C:Genetics:
A:Gene: L1439.2
A:Map position: 1

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Query Match 2.8%; Score 104; DB 2; Length 1487;
Best Local Similarity 23.7%; Pred. No. 15;
Matches 63; Conservative 19; Mismatches 112; Indels 72; Gaps 9;

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QY 444 PMDKYIHKRWALVWLACILLFAAALSLLKLDHAKAAAGRAALLLYSADDSGFERLYG 503
Db 19 PLDAQGH-----VCHARAATAPATVVSNAEVTGARGSCAPLHASREDT--RDRDS 68
QY 504 ALASALCQLPLRVAVDLWSRR-----ELSAQGPVAMFHAQRQTL-----QEGGVVLL 552
Db 69 PVAAPQOQPALNAEDEWRWRASRPASSASSSSPSAQDEAHSRVDVYEDGQGG----- 123
QY 553 FSPCAVALCSEWLQDGVGPGCAHCPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHP 612
Db 124 --EEAADRSEWRHS-----GADGASDDAEASSSTA-----LHP 155
QY 613 DAVPALFRTPVFTLP SOLPDLGALQOPRAPRSRQERAEQVSRALQPALDSYFHPPG 672
Db 156 PSPQLHQEASPLPLSLTPVATACTQOAKPP-----STTAPPGLESDTTPPPQ 203
QY 673 TPAPGRGVGP-----GAGPGAGDGT 692
Db 204 VVSQKGKTDPAKRCLCTAVAPASGRAT 229

Search completed: February 24, 2003, 09:23:35
Job time : 58 secs

Result No.	Query No.	Score			Match		Length	DB	ID	Description
		Score	Match							
1	1	173	4.7	866	1	I17R_HUMAN	Q95f46	homo sapien		
2	2	165	4.4	864	1	I17R_MOUSE	Q60943	mus musculus		
3	3	137.5	3.7	3707	1	PGBM_MOUSE	Q50793	mus musculus		
4	4	118.5	3.2	1711	1	PTPO_RAT	Q64612	rattus norv		
5	5	113.5	3.1	761	1	POQF_KLEPN	P27508	klebsiella		
6	6	112.5	3.0	1208	1	RCQ4_HUMAN	O94761	homo sapien		
7	7	108.5	2.9	925	1	W70T_HUMAN	P57737	homo sapien		
8	8	107	2.9	825	1	IL4R_HUMAN	P24394	homo sapien		
9	9	107	2.9	2003	1	NTC4_HUMAN	O99466	homo sapien		
10	10	104.5	2.8	975	1	CUT1_CANFA	P39881	canis famli		
11	11	103.5	2.8	676	1	UL06_HSV11	P10190	herpes simp		
12	12	102	2.7	922	1	W70T_MOUSE	Q9d2v7	mus musculus		
13	13	101.5	2.7	1151	1	ATCF7_YEAST	P40527	saccharomyc		
14	14	100.5	2.7	753	1	UL06_HSVB6	P28944	equine herp		
15	15	100.5	2.7	3312	1	CLR3_HUMAN	O9pvy7	homo sapien		
16	16	99	2.7	955	1	CHRD_HUMAN	Q9h2x0	homo sapien		
17	17	99	2.7	1011	1	M3K6_HUMAN	O95382	homo sapien		
18	18	98.5	2.7	546	1	RAAS_MOUSE	P58742	mus musculus		
19	19	98.5	2.7	587	1	ND2C_RAT	P70545	rattus norv		
20	20	98.5	2.7	741	1	TLE4_RAT	Q07141	rattus norv		
21	21	98.5	2.7	766	1	TLE4_HUMAN	Q04727	homo sapien		
22	22	98.5	2.7	766	1	TLE4_MOUSE	Q62441	mus musculus		
23	23	98.5	2.7	948	1	CHRD_MOUSE	Q9z0e2	mus musculus		
24	24	98.5	2.7	1505	1	CUT1_HUMAN	P39880	homo sapien		
25	25	98.5	2.7	1524	1	Y133_HUMAN	Q14146	homo sapien		
26	26	98	2.6	1487	1	ICP4_HSVB6	P28925	equine herp		
27	27	98	2.6	1487	1	ICP4_HSVBK	P17473	equine herp		
28	28	98	2.6	2205	1	POLN_RSVBT	P13889	rubella vir		
29	29	97.5	2.6	418	1	NER3_RAT	O99pw5	rattus norv		
30	30	97.5	2.6	850	1	NRG2_HUMAN	O14511	homo sapien		
31	31	97.5	2.6	4393	1	PGBM_HUMAN	P98160	homo sapien		
32	32	97	2.6	2594	1	7LES_DROVI	P20806	drosophila		
33	33	96.5	2.6	392	1	GAG_BLAU	P25058	bovine leuk		


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FT:  DOMAIN 2620 2720  IG-LIKE C2-TYPE DOMAIN 12.
FT:  DOMAIN 2721 2809  IG-LIKE C2-TYPE DOMAIN 13.
FT:  DOMAIN 2810 2895  IG-LIKE C2-TYPE DOMAIN 14.
FT:  DOMAIN 2896 2980  IG-LIKE C2-TYPE DOMAIN 15.
FT:  DOMAIN 2984 3162  LAMININ G-LIKE 1.
FT:  DOMAIN 3163 3241  EGF-LIKE.
FT:  DOMAIN 3245 3425  LAMININ G-LIKE 2.
FT:  DOMAIN 3518 3705  LAMININ G-LIKE 3.
FT:  SITE -65 67  HEPARAN SULFATE (POTENTIAL).
FT:  SITE 71 73  HEPARAN SULFATE (POTENTIAL).
FT:  SITE 76 78  HEPARAN SULFATE (POTENTIAL).
FT:  SITE 3615 3617  MEDIATES MOTOR NEURON ATTACHMENT
                                (POTENTIAL).
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FT:  DISULFID 2170 2215  BY SIMILARITY.
FT:  DISULFID 2268 2313  BY SIMILARITY.
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FT:  DISULFID 2456 2506  BY SIMILARITY.
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FT:  DISULFID 2641 2686  BY SIMILARITY.

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Query Match 3.7%; Score 137.5; DB 1; Length 3707;
Best Local Similarity 19.5%; Pred. No. 0.034;
Matches 163; Conservative 73; Mismatches 235; Indels 365; Gaps 42;
Qy 4 PWFLLSLALGRSPVVLRLVGPQDQAT-----HCSP-----GLSC---- 39
Db 272 PQLFLSPVGPFS-----ACGPQBSCHGHCIPRDYLCDDGQEDCDRCDSDELGCASPP 323

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QY 40 -----RLWSDILCLPGDI-----VPAPGPVLAPTHLQTEL 71
DB 324 PCEPNEFACENGCHALKLRCD-----GDFDCEDRTDEANCSVKQPGCEVCGPTHFCQVST 378
QY 72 LR-----CQKETDCDCLRLVAVHLAVHGHWEPEDEKFGGAADSGVEEPNLSLOAQ 124
DB 379 NRCIPASFHCDESDC-----PDRSDEFGCMPPQVVVTPPOQ-SIQA- 418
QY 125 VVLSFQAYPTARCVLLEVQVPAALVQFGOSVGSVVYDCEFAALGSEVRIWSYTPRYEKE 184
DB 419 -----SRGO-----TVTTCVATGVPTPIINW-----R 441
QY 185 LNHTQOLPALPWLNVSDGNDVHLVNLVSEEQHFG-----LSLYW 224
DB 442 LN-WGHIPAHPRVMTSEGGRTLIIRDYKEADOGAYTCAMNSRGMVFGIPDGVLELV- 499
QY 225 NOVQGPCKPRWHKNTLGPQIITLNHTDLVPCICIQWPLEPDSVRTNICP-----FREDPR 280
DB 500 --PQRGPCPDGHFYLE-----DSASCLPCFCFGV-----TNVCSSLRFRDQIR 541
QY 281 A---HQNWLQAAARLLTLQSWLLLDAPCSLPAEAALCWAPGDPQCPPLVPPLSWENVTV 337
DB 542 LSFQDPNDFKGVNTM-----PSQPGVPPPLSSTQLQI 573
QY 338 DKVL-EFPLLKHPNLCVOVNSSEKLOELWA-----DSLQ----- 374
DB 574 DPALQEFQL-----VDLSRRLVHDATWALPKQFLGNKVDSYGGFLRYKRYELA 623
QY 375 -----PL-KDDVLL-----LETRGPQDNRSLSALEPSGCTSLPSKASTRAARLGYLLQ 422
DB 624 RGMLEPVQKPDVILVGAGYRLHSRGTPTH-----PGTLNQRQVQLSE---- 666
QY 423 DLQSGCQLQWDDDLGALWACPMQKYIHKRWALVWLACLLFA-AALSLILLKKHAKAA 481
DB 667 -----EHWVHESGRPVQRAEMLOALASLEAVLLQVYNTKMA 703
QY 482 ARGRAALLYSADDSGFERLVGALASAL--COLPLRVAVDLNSRRELSAAGPVAVHQAOR 539
DB 704 SVGLSDIWN---DTVTHTTHIGHRAHSVEECRPIGYS-----GLSCSDAHF---- 749
QY 540 ROTLQEGGVVLLFS-----PGAVALC-----SEWLQDGVSGPGAHGPHDAFR 582
DB 750 --TRVPGGYPYLGTCSCNCGNHASSCDPVYGHCLNCQHNTGEGQCDKCKPFGF--DAYK 805
QY 583 ASLSCVLPDFLOGRAPGSYVGA-----CFDRLLHPDAVPALFRTVPVFT---LPSQLP 632
DB 806 ATATACRP-----CPCPYIDASRRFSDTCF---LDTDQATCDACAPGYTGRCCSCAP 856
QY 633 DFLGALQOP-----RAPRSGRLQRAEQ-----VSRALQPALDSYFH 669
DB 857 GYEGNPIQPGGKCRPTTOEIVRCDERGSLGTSGETCRKNVNVVGLNCNCSGDSGFH 912

RESULT 4
PTPO_RAT
ID PTPO_RAT STANDARD; PRT; 1711 AA.
AC Q64612;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Osteotesticular protein tyrosine phosphatase precursor (EC 3.1.3.48)
DE (OSr-PTP).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Osteosarcoma;
RX MEDLINE=95074080; PubMed=7527035;
RA Mauro L.J., Olmsted E.A., Skrobacz B.M., Mourey R.J., Davis A.R.,
RA Dixon J.E.;
RT "Identification of a hormonally regulated protein tyrosine

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DR	MIM: 268400; --	
DR	InterPro; IPR001410; DEAD.	
DR	InterPro; IPR001650; Helicase_C.	
DR	InterPro; IPR004589; RecQ.	
DR	InterPro; IPR001878; Znf_CCHC.	
DR	Pfam; PF00270; DEAD; 1.	
DR	Pfam; PF00271; Helicase_C; 1.	
DR	SMART; SM00487; DEXDC; 1.	
DR	SMART; SM00490; HELICC; 1.	
DR	SMART; SM00343; Znf_C2HC; 1.	
DR	TIGRFAMS; TIGR00614; rescq; 1.	
KW	Hydrolase; Helicase; ATP-binding; Nuclear protein.	
FT	NP_BIND 502 509 ATP (POTENTIAL).	
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SQ	SEQUENCE 1208 AA; 133076 MW; CB809A7765AB48A1 CRC64;	
Query Match 3.08; Score 112.5; DB 1; Length 1208;		
Best Local Similarity 19.68; Pred. No. 0.76;		
Matches 115; Conservative 73; Mismatches 194; Indels 205; Gaps 31;		
Qy	16 PVVLSRLVGPQDATHCGSPGLSC---RLWSDIL--CLPGDIVPACPVLPVLA ^{THLQ} ---	67
Db	619 PCYLRVCKVLRRCMGVCH ^{FLG} LITATARTASDVQAHLVAEEFDLHGPAVPV ^{TNLHLSV} 678	
Qy	68 -----TELVRCKETCDCLCRVA ^{VHL} --AVHGWEEPEDEE 103	
Db	679 SMDRTDQALLTLQKKRFQNLSDSI ^{IYCNRRDE} ---RTAALLRTCLHAAV ^{PGS} --- 732	
Qy	104 KFGGAADSGVEEPRNASL-----QAQVVLSPQAY-----PTARC ^{VLLV} 142	
Db	733 --GGRAPKTTAEAYHAGMC ^{SRERRVQRAFMQGLRVVAVTAF} GMGLDRPD ^{VRV} --LHL 789	
Qy	143 QVPAALVQFGSGSVVYDCEFAALGSEVR ^{TWS} TOPRYE--KELNHTQQLPALP ^{WLNV} 200	
Db	790 GLPSPFSFYQAVGRGD-----GQPAHCHLFLQPGEDLRELRRH ^{VHAD} STDFLAV ^K 843	
Qy	201 ADGDNVHLVLNV-----SEQHFGSLSYNQVQCP-PKPRW-----HKN 238	
Db	844 -----RLVQRVPFAC ^{TCTCT} TRPSEGE-----GAVGERPVKY ^{PQEAQLSHQA} 889	
Qy	239 LTGPQIITLNTDLVPC-LCIQWPLEPDSV ^{RNIC} PFREDPRAHONLQAA ^{RLL} --T 295	
Db	890 APGPRRCVMGHERALPQLT ^{QALDMP} EEAETLLCYL---ELH ^{PHHW} ---LELLAT ^T 941	
Qy	296 LQSWLLDAPCSLPAEALCW ^{RAP} -----GGDPCQ-----PLVPPL ^{SHENV} 335	
Db	942 YTHCLRLNCPGPAQLQALAH ^{RCP} PLAVCLAQQLPEDPGQSSSVFDMVK ^{LVD} SMGWE ^{LA} 1001	
Qy	336 TVDKVL-----EPLLKH ^{PNLCVQVNS} SEKQLQEQCLWADSLG 374	
Db	1002 SVRRALCOLQNDHEPRTG ^{VRRGT} CVLVEFSELAFLH ^{RS} PGDLTAEK ^{DQ} ICDFLY----G 1057	
Qy	375 PLKDDVLLLETRGPQDN ^{RNS} ICALB-----PSGCTSLPSKA ^{STRAR} ----LGEY 419	
Db	1058 RVQ-----ARERQALARL ^{RRT} QAFHSVAFPPSCG ^{PCLE} QDEERSTR ^{LK} DLG ^{RGY} 1107	
Qy	420 L-----LQDLQS---GQC-LQLWDDDLGALWAC ^{PMK} YIHR 452	
Db	1108 FEEEGGPGGMEDAQGP ^{EQAR} LQDWEDQV----RCDIRQ ^{FL} SLR 1150	
RESULT 7		
W70T_HUMAN		
ID	W70T_HUMAN	STANDARD; PRT; 925 AA.
AC	P57737;	
DT	16-OCT-2001 (Rel. 40, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	70 kDa WD-repeat tumor rejection antigen homolog.	
OS	Homo sapiens (human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI	TaxID:9606;	

QY 439 ALWACPMKXIIHKRWALVWLACLLFAAALLSKLLKKHAKAAARGRAALLYSADDSGF 498
Db 469 -----PSSKFRHAQGT-----VLHRDSHITNLKG--LNLTTFGESDGF 504
QY 499 ERLVGALGALSALCOLPURVAVDVLWSRRLSAOGPVAVFHAQR-----ROTLQEGGVVV 550
Db 505 -----CANKURVAVPL-----LSSGGQVAVLELRKPGRLPDTALPTLQNGAAVT 548
QY 551 LL-----FSPCAVALCSE 563
Db 549 DLAWDPDPHRLAVAGE 565

RESULT 8
IL4R_HUMAN
ID IL4R_HUMAN STANDARD; PRT; 825 AA.
AC P24394; Q96P01;
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE Interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124 antigen).
GN IL4R OR IL4RA OR 582J2.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RX MEDLINE=90171849; PubMed=2307934;
RA Idzerda R.L., March C.J., Mosley B., Lyman S.D., Bos T.V.,
RA Gimpel S.D., Din W.S., Grabstein K.H., Widmer M.B., Park L.S.,
RA Cosman D., Beckmann M.P.;
RT "Human interleukin 4 receptor confers biological responsiveness and
RT defines a novel receptor superfamily";
RL J. Exp. Med. 171:861-873(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91120547; PubMed=2278997;
RA Galizzi J.-P., Zuber C.E., Harada N., Gorman D.M., Djossou O.,
RA Kastelein R., Banchereau J., Howard M., Miyajima A.;
RT "Molecular cloning of a cDNA encoding the human interleukin 4
RT receptor";
RL Int. Immunol. 2:669-675(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99425270; PubMed=10493829;
RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from
RT human chromosome 16p and 16q";
RL Genomics 60:295-308(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RN Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP VARIANTS VAL-75; ALA-400; ARG-431; LEU-436 AND PRO-786.
RX MEDLINE=97224413; PubMed=9070874;
RA Deichmann K., Bardutzky J., Forster J., Heinzmann A., Kuehr J.;
RT "Common polymorphisms in the coding part of the IL4-receptor gene";
RL Biochem. Biophys. Res. Commun. 231:696-697(1997).
RN [6]
RP VARIANT ATOPIC ARG-576.
RX MEDLINE=98041803; PubMed=9392697;
RA Hershey G.K.K., Friedrich M.F., Esswein L.A., Thomas M.L.,
RA Chatila T.A.;
RT "The association of atopy with a gain-of-function mutation in the

alpha subunit of the interleukin-4 receptor."; New Engl. J. Med. 337:1720-1725(1997).
RN [7]
RP VARIANT ATOPIC ASTHMA VAL-75.
RX MEDLINE=98282087; PubMed=9620765;
RA Mitsuyasu H., Izuhara K., Mao X.-O., Gao P.S., Arinobu Y., Enomoto T.,
RA Matsui M., Sasaki S., Dake Y., Hamasaki N., Shirakawa T., Hopkin J.M.;
RT "Ile50Val variant of IL4R alpha upregulates IgE synthesis and
RT associates with atopic asthma";
RL Nat. Genet. 19:119-120(1998).
RN [8]
RP VARIANT ATOPIC ASTHMA VAL-75.
RX MEDLINE=99322293; PubMed=10390422;
RA Noguchi E., Shibasaki M., Arinami T., Takeda K., Yokouchi Y.,
RA Kobayashi K., Imoto N., Nakahara S., Matsui A., Hamaguchi H.;
RT "No association between atopy/asthma and the Ile50Val polymorphism of
RT IL-4 receptor";
RL Am. J. Respir. Crit. Care Med. 160:342-345(1999).
RN [9]
RP VARIANTS PRO-503 AND ARG-576.
RX MEDLINE=99250314; PubMed=10233717;
RA Kruse S., Japha T., Tedner M., Sparholt S.H., Forster J., Kuehr J.,
RA Deichmann K.A.;
RT "The polymorphisms S503P and Q576R in the interleukin-4 receptor alpha
RT gene are associated with atopy and influence the signal
RT transduction";
RL Immunology 96:365-371(1999).
RN [10]
RP VARIANT ALA-752.
RX MEDLINE=20143377; PubMed=10677312;
RA Ober C., Leavitt S.A., Tsalenko A., Howard T.D., Hoki D.M., Daniel R.,
RA Newman D.L., Wu X., Parry R., Lester L.A., Solway J., Blumenthal M.,
RA King R.A., Xu J., Meyers D.A., Bleecker E.R., Cox N.J.;
RT "Variation in the interleukin 4-receptor alpha gene confers
RT susceptibility to asthma and atopy in ethnically diverse
RT populations";
RL Am. J. Hum. Genet. 66:517-526(2000).
RN [11]
RP VARIANT ATOPIC ARG-576.
RX MEDLINE=20269830; PubMed=10809862;
RA Oiso N., Fukui K., Ishii M.;
RT "Interleukin 4 receptor alpha chain polymorphism Gln551Arg is
RT associated with adult atopic dermatitis in Japan";
RL Br. J. Dermatol. 142:1003-1006(2000).
RN [12]
RP VARIANT PRO-786.
RX MEDLINE=21405389; PubMed=11513543;
RA Andrews R.P., Burrell L., Rosa-Rosa L., Cunningham C.M.,
RA Brzezinski J.L., Bernstein J.A., Khurana Hershey G.K.;
RT "Analysis of the Ser786Pro interleukin-4 receptor alpha allelic
RT variant in allergic and nonallergic asthma and its functional
RT consequences";
RL Clin. Immunol. 100:298-304(2001).
RN [13]
RP VARIANT ILE-579.
RX MEDLINE=21182061; PubMed=11285129;
RA Lozano F., Places L., Villa J.M., Padilla O., Arman M., Gimferrer I.,
RA Suarez B., Lopez de la Iglesia A., Miserachs N., Vives J.;
RT "Identification of a novel single-nucleotide polymorphism (Val554Ile)
RT and definition of eight common alleles for human IL4RA exon 11";
RL Tissue Antigens 57:216-220(2001).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR INTERLEUKIN-4. A SOLUBLE FORM
CC OF THE IL-4 RECEPTOR MAY REPRESENT A REGULATORY MOLECULE SPECIFIC
CC FOR IL-4-DEPENDENT IMMUNE RESPONSES.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA CHAIN AND A COMMON GAMMA CHAIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DISEASE: DEFECTS IN IL4R ARE A CAUSE OF ATOPIC ASTHMA.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD124 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd124.htm".
CC -----
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CC EMBL; X52425; CAA36672.1; -
 CC EMBL; AC004525; AAC23495.1; -
 CC EMBL; AF421855; AAL12163.1; -
 CC PIR; A60386; A60386.
 CC PIR; A47603; A47603.
 CC GenBank; HGNC:6015; IL4R.
 CC MIM; 147781; -
 CC InterPro; IPR002996; CRIA.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR003531; Hemtopoptn_S_F1.
 CC SMART; SM0060; FN3; 1.
 CC PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Disease mutation;
 KW Polymorphism.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 825 INTERLEUKIN-4 RECEPTOR ALPHA CHAIN.
 FT DOMAIN 26 232 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 233 256 POTENTIAL.
 FT DOMAIN 257 825 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 34 44 BY SIMILARITY.
 FT DISULFID 74 86 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 75 75 I -> V (IN ATOPIC ASTHMA).
 FT VARIANT 400 400 /FTIG=VAR_008034.
 FT VARIANT 431 431 E -> A (IN DBSNP:1805011).
 FT VARIANT 436 436 C -> R (IN DBSNP:1805012).
 FT VARIANT 436 436 S -> L (IN DBSNP:1805013).
 FT VARIANT 503 503 /FTIG=VAR_011659.
 FT VARIANT 503 503 S -> P (IN DBSNP:1805015).
 FT VARIANT 576 576 /FTIG=VAR_011660.
 FT VARIANT 579 579 Q -> R (IN ATOPIC PATIENTS).
 FT VARIANT 579 579 V -> I.
 FT VARIANT 752 752 /FTIG=VAR_011661.
 FT VARIANT 786 786 S -> A (IN DBSNP:1805016).
 FT VARIANT 786 786 S -> P (IN 1.8% OF THE POPULATION; IN DBSNP:1805014).
 FT SEQUENCE 825 AA; 89658 MW; 9F886DF5612297F8 CRC64;
 Query Match 2.9%; Score 107; DB 1; Length 825;
 Best Local Similarity 19.2%; Pred. No. 1.3;
 Matches 155; Conservative 66; Mismatches 284; Indels 304; Gaps 36;
 QY 41 LWDSDILGLGDIVP-----APGVLAPTHLQTELVLRCOKETDCDCLRLVAVHLAVH 93
 DB 103 LWAGQQLLWKGSKFSEHKPRAPGNLTHTVNTVDTLLTWSNPPYDPDNYLYNHLTVAVN 162
 QY 94 GHWEPEDEERFGGAADSGVEEPRNASLQAOVVLFOAYPTARCILLE--VQVPAALVQF 151
 DB 163 -IWSENDPAD-----FRIY---NVTYLEPSLRIAASTLKS 193
 QY 152 GQSVGVVYDCFEAALGSEVRIWSTQPRYKELNHTQOLPALPWLNVSDAGDNVHLVLN 211
 DB 194 GIS-----YRVRVWAQCY-----NTWSEWSPSTKWHNSYREPEQHLHLG 236
 QY 212 VSEBOHFGLSL-----YWNQVQGPKKP-----WHKNLFGPOI 244
 DB 237 VSVSCIVILAVCLLCYVSTIKKEMWDDIIPNARSRLVAILIQAQGSQWEKRSRGQEP 296

QY 245 ITLNH-----TDLVPLCLCIQWPLEPDSVRTNICPPREDPRAHQNLMQAARLLTLQSW 299
 DB 297 AKCPHMKNLTKLLPCF-----LEHMKRD-----EDPH-----KAA--KEMPPQGS 336
 QY 300 LLDAPCSLPAEALCWAPGDCQPLVPLSWENVTVDKVLFEPL-----LKGH 349
 DB 337 GKSAMCPVEISKTVLW-----PESISVRCVLFELFEAPVECEEEVEBEK- 382
 QY 350 PNLQVQVNSSEK-----LQLOECIWAQSLGKPLKDDVLLLETRG-----PDNRSILCA 396
 DB 383 -SFCASPESSRDDFOEGREGIVARLTFESFLDLIG-----EENGFGCOQDMGESCL 432
 QY 397 LEPSGCTS-----LPSKASTRAARLGEYLLQDLSQGCQLQWLWDDDLGALWACPMDKYI 449
 DB 433 LPSPGSTSAHMPWDEPPSAGPKAPPWK-----EQPLHLEPSPASPTSPDN--- 481
 QY 450 HRRWALVWIACLLFAAALSILLKLDHAKAAAGRAALLLYSADDSGFERLYGALASAL 509
 DB 482 -----LTC-----TETPLVIAGNPAYRFSNSLSQSP 508
 QY 510 COLPLRVAVDLNRSRELS-----AQPVAWFHQAORROTLOEGVVV 550
 DB 509 C--PRELGPDLARHLEVEPEMPCVPOLSEPTTVQPEPETWEQILRRNVLQHGAAAA 566
 QY 551 LLFSP--GAVALCSEWLQDGV-----GPGAHGPHDAFRASL---SCVLPDFLQ--GRAP 598
 DB 567 PVSATSGYQEFVHVEQGGTQASAVVGLPGGEAGYKAFSSLLASSAVSPEKCGFGASS 626
 QY 599 GSYVGACFDRL-----HPDAVPALFTVPVET-----LPSQLPDFLGA- 637
 DB 627 GEEGYKFDQLLPGCGDPAPVP-----VPLTFGLDREPPSPQSHLPSSSPEHLGLE 681
 QY 638 -----LQOPRAPS-----GRLOERAQVSRALQPALDS 666
 DB 682 PGEKVEDMPKPLPQEQATDPLVDSLGSIVYSALTCHLCHLQKHQCHGQEDGQTPVMAS 741
 QY 667 -----YFHPGCTPAPRGVGGCAGP 686
 DB 742 PCCGCCCGDRSSPPTTTLRAPDPSGGVP 770
 RESULT 9
 NTC4_HUMAN
 ID NTC4_HUMAN STANDARD; PRT: 2003 AA.
 AC Q99466; Q00306; Q9940; Q99458; Q9H358; Q9U119; Q9U1J0;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)
 DE (hNotch4).
 GN NOTCH4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND POLYMORPHISM OF POLY-LEU.
 RC TISSUE=Placenta;
 RX MEDLINE=97311416; PubMed=9168133;
 RA Sugaya K., Sasanuma S.-I., Nohata J., Kimura T., Fukagawa T.,
 RA Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.;
 RT "Gene organization of human NOTCH4 and (CTG)n polymorphism in this
 RT human counterpart gene of mouse proto-oncogene Int3.";
 RL Gene 189:235-244(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE=Bone marrow, and Heart;
 RX MEDLINE=98360091; PubMed=9693032;
 RA Li L., Huang G.M., Banta A.B., Deng Y., Smith T., Dong P.,
 RA Friedman C., Chen L., Trask B.J., Spies T., Rowen L., Hood L.;
 RT "Cloning, characterization, and the complete 56.8-kilobase DNA
 RT sequence of the human NOTCH4 gene.";

Genomics 51:45-58(1998).
 [3] SEQUENCE OF 1-503 FROM N.A., AND VARIANTS GLN-117 AND GLN-317.
 RA Miyagawa T., Tokunaga K., Hojho H.;
 RT "Human notch4 gene variant."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP IDENTIFICATION OF LIGANDS.
 RX MEDLINE-99180765; PubMed-10079256;
 RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Catcangiu M.-L.,
 RT Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
 RL "Human ligands of the Notch receptor."
 CC Am. J. Pathol. 154:795-794(1999).
 CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands
 CC Jagged1, Jagged2 and Delta to regulate cell-fate determination.
 CC Upon ligand activation through the released notch intracellular
 CC domain (NICD) it forms a transcriptional activator complex with
 CC RBP-J kappa and activates genes of the enhancer of split locus.
 CC Affects the implementation of differentiation, proliferation and
 CC apoptotic programs. May regulate branching morphogenesis in the
 CC developing vascular system (By similarity).
 CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
 CC terminal fragment N(EC) which are probably linked by disulfide
 CC bonds (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following
 CC proteolytical processing NICD is translocated to the nucleus.
 CC -!- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; may be
 CC produced by alternative splicing.
 CC -!- TISSUE SPECIFICITY: Highly expressed in the heart, moderately in
 CC the lung and placenta and at low levels in the liver, skeletal
 CC muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow
 CC and fetal liver. No expression was seen in adult brain or
 CC peripheral blood leukocytes.
 CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 CC which is proteolytically cleaved by a furin-like convertase in the
 CC trans-Golgi network before it reaches the plasma membrane to yield
 CC an active, ligand-accessible form. Cleavage results in a C-
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme
 CC (TACE) to yield a membrane-associated intermediate fragment called
 CC notch extracellular truncation (NEXT). This fragment is then
 CC cleaved by presenilin dependent gamma-secretase to release a
 CC notch-derived peptide containing the intracellular domain (NICD)
 CC from the membrane (By similarity).
 CC -!- PTM: Phosphorylated (By similarity).
 CC -!- POLYMORPHISM: The poly-Leu region of NOTCH4 (in the signal
 CC peptide) is polymorphic and the number of Leu varies in the
 CC population (from 6 to 12).
 CC -!- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -!- SIMILARITY: CONTAINS 28 EGF-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
 CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
 CC in position 1438 to 1463.
 CC
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 CC use by non-profit institutions as long as its content is in no way
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 CC
 CC EMBL: D63395; BAA09708.1; ALT_FRAME.
 CC EMBL: D86566; BAA13116.1; -
 CC EMBL: U95299; AAC32288.1; -
 CC EMBL: U89335; AAC63097.1; -
 CC EMBL: AB023961; BAB20317.1; -
 CC EMBL: AB024520; BAB88951.1; -
 CC EMBL: AB024578; BAB88952.1; -
 CC HSSP: P08709; 1BF9.
 CC Genew: HGNC:7884; NOTCH4.
 CC MIM: 164951; -

InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR000800; Notch.
 DR Pfam; PF00008; EGF; 26.
 DR Pfam; PF00023; ank; 6.
 DR Pfam; PF00066; notch; 2.
 DR PRINTS; PR00010; EGFBL00D.
 DR PRINTS; PR00011; EGFAMININ.
 DR PRINTS; PR00012; FNTYPEI.
 DR SMART; SM00248; ANK; 5.
 DR SMART; SM00179; EGF_CA; 11.
 DR SMART; SM00001; EGF_Like; 15.
 DR SMART; SM00004; NL; 2.
 DR PROSITE; PS50088; ANK_REPEAT; 5.
 DR PROSITE; PS50297; ANK_REP_REGION; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 11.
 DR PROSITE; PS00022; EGF_1; 28.
 DR PROSITE; PS01186; EGF_2; 21.
 DR PROSITE; PS01187; EGF_CA; 9.
 KW Receptor; Transcription regulation; Activator; Differentiation;
 KW Developmental protein; Repeat; ANK repeat; EGF-like domain;
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism;
 KW Triplet repeat expansion; Alternative splicing.
 FT SIGNAL 1 23
 FT CHAIN 24 2003
 FT CHAIN 1432 2003
 FT CHAIN 1467 2003
 FT CHAIN 1447 2003
 FT CHAIN 1448 1468
 FT TRANSMEM 1469 2003
 FT DOMAIN 24 63
 FT DOMAIN 64 115
 FT DOMAIN 118 155
 FT DOMAIN 156 192
 FT DOMAIN 194 232
 FT DOMAIN 234 274
 FT DOMAIN 276 312
 FT DOMAIN 314 353
 FT DOMAIN 355 391
 FT DOMAIN 392 430
 FT DOMAIN 432 473
 FT DOMAIN 475 511
 FT DOMAIN 513 549
 FT DOMAIN 551 587
 FT DOMAIN 589 625
 FT DOMAIN 626 659
 FT DOMAIN 661 689
 FT DOMAIN 691 727
 FT DOMAIN 729 765
 FT DOMAIN 767 803
 FT DOMAIN 806 842
 FT DOMAIN 844 880
 FT DOMAIN 882 928
 FT DOMAIN 930 966
 FT DOMAIN 968 1004
 FT DOMAIN 1006 1044
 FT DOMAIN 1046 1085
 FT DOMAIN 1087 1126
 FT DOMAIN 1130 1171
 FT DOMAIN 1172 1476
 FT REPEAT 1165 1212
 FT REPEAT 1213 1246
 FT REPEAT 1247 1286
 FT REPEAT 1633 1665
 FT REPEAT 1666 1698
 FT REPEAT 1700 1732
 FT REPEAT 1733 1765
 DOMAIN 1447 2003
 EXTRACELLULAR DOMAIN (BY
 SIMILARITY).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 EGF-LIKE 1.
 EGF-LIKE 2.
 EGF-LIKE 3.
 EGF-LIKE 4.
 EGF-LIKE 5.
 EGF-LIKE 6.
 EGF-LIKE 7.
 EGF-LIKE 8.
 EGF-LIKE 9.
 EGF-LIKE 10.
 EGF-LIKE 11.
 EGF-LIKE 12.
 EGF-LIKE 13.
 EGF-LIKE 14.
 EGF-LIKE 15.
 EGF-LIKE 16.
 EGF-LIKE 17.
 EGF-LIKE 18.
 EGF-LIKE 19.
 EGF-LIKE 20.
 EGF-LIKE 21.
 EGF-LIKE 22.
 EGF-LIKE 23.
 EGF-LIKE 24.
 EGF-LIKE 25.
 EGF-LIKE 26.
 EGF-LIKE 27.
 EGF-LIKE 28.
 EGF-LIKE 29.
 POLY-ARG.
 LIN/NOTCH 1.
 LIN/NOTCH 2.
 LIN/NOTCH 3.
 ANK 1.
 ANK 2.
 ANK 3.
 ANK 4.

```
FT REPEAT 1766 1798 ANK 5.
FT DISULFID 28 41 BY SIMILARITY.
FT DISULFID 35 51 BY SIMILARITY.
FT DISULFID 53 62 BY SIMILARITY.
FT DISULFID 68 80 BY SIMILARITY.
FT DISULFID 74 103 BY SIMILARITY.
FT DISULFID 105 114 BY SIMILARITY.
FT DISULFID 122 133 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 145 154 BY SIMILARITY.
FT DISULFID 160 171 BY SIMILARITY.
FT DISULFID 165 180 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 198 211 BY SIMILARITY.
FT DISULFID 205 220 BY SIMILARITY.
FT DISULFID 222 231 BY SIMILARITY.
FT DISULFID 238 249 BY SIMILARITY.
FT DISULFID 243 262 BY SIMILARITY.
FT DISULFID 264 273 BY SIMILARITY.
FT DISULFID 280 291 BY SIMILARITY.
FT DISULFID 285 300 BY SIMILARITY.
FT DISULFID 302 311 BY SIMILARITY.
FT DISULFID 318 332 BY SIMILARITY.
FT DISULFID 326 341 BY SIMILARITY.
FT DISULFID 343 352 BY SIMILARITY.

Query Match 2.9%; Score 107; DB 1; Length 2003;
Best Local Similarity 21.8%; Pred. No. 4;
Matches 176; Conservative 62; Mismatches 251; Indels 320; Gaps 46;

QY 32 HCSPLGSLR-----WSDIILCGDIVPAPGP-----VLAPTHQTELVLRCQKETDCD 81
DB 1267 HCEKG--CNTAECGWGGD--CRPEDGDPWGPSALLWLSPALDQOLFALRV---LS 1320

QY 82 LCLRAVHLAVGHWEPE-----DEEFGGAADSGVEPRNASLOAQ--- 124
DB 1321 LTLRV-----GLWVRKORDGDMVYPYPGARAEKLGTRDTYQE--RAAPQTQPLG 1371

QY 125 -----VYLSFQA-----YPTARCV-----LLEVOVPAALVQ 150
DB 1372 KETDLSLGSFVVMGVYDLSRCPDHPASRCPWDPGLLLRFLAAMAVALPLUGPLLA 1431

QY 151 FQSGVG-----SVYDCEFAALGSEV-----RIW---SYTQPR 180
DB 1432 VHPHAGTAPPANOLPWPVLCSPPVAGVILLALGALLVLQIRRRRERHAGLWLPGFTRP 1491

QY 181 YEKELNHTQOLP-----ALPWLNSADGNVHLVNVSEEHFGLSYNWQVGPSPK-- 232
DB 1492 RTQSAPHRRRPLGSDSIGLKALKPKAEVDEDCGVVMCSGPPE--GEVGOAEETGPPSTC 1549

QY 233 -----PRWHKNTGPOIITLNHTDLVPCL---CIOV-----W 261
DB 1550 QLWSLSGGCGALPQAAMLTPPOESEMEAFDTRGPDGVTPPLMSAVCCGEVQSGTFQGA 1609

QY 262 -----PLEPDSVRTNICPFREDPRAH-----ONLQAAARLRLTLQSWLLDAPCSLP 310
DB 1610 LGCPEPWEV-LLDGGAC-----PQAHTVGTGETPLHAAFRSPTAARRLLEA----- 1656

QY 311 RALCHRAPGGDCQPLVPPLSWENVTVDKLEPPLKHPNLCVQVNSSEKQLQECLEWA 370
DB 1657 -----GANPNQ-----DRAGRTPL-----HAAVAADAREVCO----- 1684

QY 371 DSLGPKDDVLLLETRGPDNRSLCALESFGCTSLPSKASTRAARLG-EYLLQDLQSGQC 429
DB 1685 -----LLRSR-----QTAVDARTEDGTPL-----MLAARLAVEDVLELIAAQA 1725

QY 430 LQWDDDLGALWACPMWKYIKRHWALVWLACLLFAAALSILILLKKDHAKAAAGRAALL 489
DB 1726 -----DVGA-----RDKW--CKTALHWAAYVNNARAARSLQAGADKQADNREOTPLF 1772

QY 490 LYSADDSGFERLVGALASALCALCPRLRVAVDLWSRRELSAQGPVAFHQAQRQ-----TLQE 545
DB 1773 LAARE-----GAVEVAQLLLGLGAAREL---RDQAGLAPADVAH-QRNHWDLTLLE 1820
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```
QY 546 GGVVLLFSPGAVALCSEWLQDGVSGPAHGPHDAFRASLSCLVPLDFLQGRAPGSYVGAC 605
DB 1821 G-----AGP-----PEARHKAATPGREAGP- 1839

QY 606 FDRLLHPDAVPALERTVPTLSQLDFLGAALOOPR-----APRSGR--LQBRABQVS 657
DB 1840 FPRA-----RTVSV-----SVPPHGGGALPRCTLSAGAGPRGGGACLQARTWSVD 1885

QY 658 RALQPALDSYFHPPTPAPGRGVGPAGP 686
DB 1886 LAARGG-GAYSHCRSL-----SGVGAGGPP 1909

RESULT 10
CUT1_CANFA
ID CUT1_CANFA STANDARD; PRT; 975 AA.
AC P39881;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CCAAT displacement protein (Homeobox protein Clox) (Clox-1)
DE (Fragment).
GN CUT1 OR CLOX.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart ventricle;
RX MEDLINE=93161940; PubMed=1363085;
RA Andres V., Nadal-Ginard B., Mahdavi V.;
RT "Clox, a mammalian homeobox gene related to Drosophila cut, encodes
RT DNA-binding regulatory proteins differentially expressed during
RT development.";
RL Development 116:321-334(1992).
CC -!- FUNCTION: DNA-BINDING REGULATORY PROTEIN, WHERE THE SMALLER
CC PROTEIN SPECIES PROBABLY REPRESENTS THE ACTIVE DNA-BINDING FORM.
CC MAY FUNCTION AS A DEVELOPMENTALLY REGULATED REPRESSOR OF TISSUE-
CC SPECIFIC GENE TRANSCRIPTION BY PREVENTING THE INTERACTION OF
CC TISSUE-SPECIFIC TRANSACTIVATORS WITH THEIR COGNATE TARGET
CC SEQUENCES. PROBABLY INVOLVED IN CELL-FATE SPECIFICATION IN DIVERSE
CC DIFFERENTIATION PROGRAMS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS: A number of isoforms may be produced by
CC alternative splicing.
CC -!- TISSUE SPECIFICITY: A BROAD PATTERN OF EXPRESSION OBSERVED IN
CC TISSUES OF DIVERSE ORIGINS, SUCH AS CARTILAGE, LIVER, BRAIN, LUNG,
CC HEART AND SKELETAL MUSCLE. THERE ARE 2 DISTINCT PROTEIN SPECIES:
CC THE LARGER ONE (230-250 KDA) IS FOUND MAINLY IN ADULT BRAIN, LUNG
CC AND HEART, AND THE SMALLER ONE (180-190 KDA) PREDOMINATES IN EARLY
CC EMBRYONIC TISSUES.
CC -!- DEVELOPMENTAL STAGE: DIFFERENTIALLY EXPRESSED DURING DEVELOPMENT.
CC SMALL PROTEIN SPECIES PREDOMINATE IN EARLY EMBRYOS AND ARE
CC UPREGULATED IN COMMITTED MYOBLASTS AND CHONDROCYTES, BUT
CC DOWN-REGULATED UPON TERMINAL DIFFERENTIATION. LARGE SPECIES ARE
CC DETECTED MAINLY IN ADULT TISSUES AND TERMINALLY DIFFERENTIATED
CC CELLS.
CC -!- DOMAIN: ASN AT POSITION 47 OF THE HOMEBOX MAY PARTICIPATE IN
CC REGULATING DNA-BINDING ACTIVITY BY PROMOTING HOMO- AND
CC HETERODIMERIZATION.
CC -!- SIMILARITY: CONTAINS 3 CUT DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CUT HOMEBOX FAMILY.
CC -----
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DR EMBL; X69017; CAA48782.1; -
DR PIR; S33121; S33121.
DR HSP; P10037; IAU7.
DR TRANSFAC; T01485; -
DR TRANSFAC; T01995; -
DR InterPro; IPR003350; Hmoob_CUT.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF02376; CUT; 3.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Transcription regulation; Homeobox; DNA-binding;
KW Developmental protein; Nuclear protein; Repeat; Repressor;
KW Coiled coil; Alternative splicing.
FT NON_TER 1
FT DNA_BIND <1 67 CUT 1.
FT DOMAIN 113 169 COILED COIL (POTENTIAL).
FT DNA_BIND 374 461 CUT 2.
FT DNA_BIND 557 644 CUT 3.
FT DNA_BIND 684 743 HOMEBOX.
SQ SEQUENCE 975 AA; 105428 MW; 724243B32C5BCFD9 CRC64;

Query Match 2.8%; Score 104.5; DB 1; Length 975;
Best Local Similarity 20.4%; Pred. No. 2.5;
Matches 174; Conservative 74; Mismatches 244; Indels 363; Gaps 44;

QY 3 VPMFLLSLALGRSPVLSLERLVGPDPATHCS-----PGLSRLWDSIILCPGDIVP 55
DB 190 IPSSPMSSVSSYPPLALSLLK---PPTAPDTSASTLPNPPALKKESQDAPGLDLPGAES 246
QY 56 APGPVLAFLHQLTELRLCQKDCDCLRLRVAVHLAVHGHWE-----PE 100
DB 247 AGS-----VLR-----HVKSELGRSGVWKDHWMSTVQPERKSAAPPE 283
QY 101 D--EEKFGAAGS-----LTQKGREFFIRMQLWLNGLGQGVLPVQGOOGPVLHS 468
DB 284 DAKSEAGGTEKKGQGHGPIAASSRDPHRRSTGRNGPALSPTPQSSELSLTGASRS 343
QY 114 EEPNASLQAO--VVLSTQAYPTARCVLLEVQVPAALVFGOSVGVYVDCFEALGSEV 171
DB 344 ETPONSPLPSSPIVPMKPAK-----SVPLTPQYEIYMYQEV 383
QY 172 RIWSTQPRYKELNHTQQLPALPWLNVSDGDNVHLVNLVSEEHQFGLSLYNQVQGP- 230
DB 384 DTIELTRQVKE-----LAKNG-----ICORIFGEKVLGLS-----QGSV 418
QY 231 -----PKPRHKNLTGPQIITLNHTDLVPLCLIQW----- 261
DB 419 SDMLSRPKP-WSK-----LTQKGREFFIRMQLWLNGLGQGVLPVQGOOGPVLHS 468
QY 262 -----PLEPDSVRTNICPFRE---DPAHQNLQAAARLRLTLOSLLDAPCSLPAEAA 312
DB 469 VTSLODPLQOCVSESTPKTSASCPAPESPMSSESVKSLT---ELVQPCP-PIET- 523
QY 313 LCWRAPGDDPCQPLVPLSWENVTVDKLEFPL-LKGHPNLVQV--VNSSEKL----- 362
DB 524 -----SKDGKPEPSPDPPAS-----DSQPATPLPUSGHSALSIQELVAMSPELDTYGITK 573
QY 363 QLQECNLWADSLGP-LKDDVLLLETRG-----PDNRSLSALPESGCTSLPSKAST 411
DB 574 RVKEVLTNNLQRLFGETILGLTQGSVSDLLSRPKPWHKLSLKREPP----- 622
QY 412 RAARLGEVLLQDSGQCLQWDDDLGALMACPMDDKYTHKRWALVWLAACLFAAALSLLIL 471
DB 623 -----VRMQLWLN-----PNN-----VEKLM 639
QY 472 LLKKDHAKAARGAALLYSADDS-----GFERLVG----- 503
DB 640 DMKREKAYMKRRHS-----SVSDSQPCPEPSVGDYSQGSAPQPHQLKPRVVLAPEE 695
QY 504 --ALASALCOLPL---RVAVDLWSRRELSSAQGPVAFWFAHQRRQTLQEGGVVLLFSPGAV 558

DB 696 KEALKRAYQOKPYPSPKTTEELATQNLKTSTVINWFHNSRIRRE----- 742
QY 559 ALCSEWLQDQVSG-PCA-HGPHDAFASLUSCVLPDFLQGRAPGSYVGAC--FDRLLHPDA 614
DB 743 -LFIEEIQAQSQGQAGARHP--SARSS-----GAAPSSGSGDCDGVAAEGPGA 789
QY 615 VPALFRTVPVFTLPQSLPDLFALGALQOPRAPRSRGRLOEAEQVSRALQPALDSYFHPGPT- 673
DB 790 ADA-EESAPAAAKSQ-----GGPAEAAVAP-----EEREE---APRPAEKRRRPRGPG 835
QY 674 PAPGRGVGPAGPGA 688
DB 836 PCPGRGGGGPAPGA 850

RESULT 11
UL06_HSV11
ID UL06_HSV11 STANDARD; PRT; 676 AA.
AC P10190;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Virion protein UL6.
GN UL6
OS Herpes simplex virus (type 1 / strain 17).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88274327; PubMed=2839594;
RA McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
RA McNab D., Perry L.J., Scott J.E., Taylor P.;
RT "The complete DNA sequence of the long unique region in the genome of
RT herpes simplex virus type 1";
RT J. Gen. Virol. 69:1531-1574(1988).
RN [2]
RP SEQUENCE OF 1-80 FROM N.A.
RX MEDLINE=88091053; PubMed=2826807;
RA McGeoch D.J., Dalrymple M.A., Dolan A., McNab D., Perry L.J.,
RA Taylor P., Challberg M.D.;
RT "Structures of herpes simplex virus type 1 genes required for
RT replication of virus DNA";
RT J. Virol. 62:444-453(1988).
CC -!- FUNCTION: PRESUMED VIRION PROTEIN; POSSIBLE ROLE IN DNA
CC PACKAGING.
CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL6,
CC EHV-1 56, EBV BHRF1, HCMV UL104, AND VZV 54.
CC -----
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CC -----
CC EMBL; D10879; BAA01652.1; -
DR EMBL; X14112; CAA32342.1; -
DR EMBL; M19119; AAA45818.2; -
DR PIR; F28133; WMBEX6.
DR InterPro; IPR002660; Herpes_UL6.
DR Pfam; PF01763; Herpes_UL6; 1.
DR ProDom; PD003210; Herpes_UL6; 1.
SQ SEQUENCE 676 AA; 74091 MW; 8CF9D73C6313FAE9 CRC64;

Query Match 2.8%; Score 103.5; DB 1; Length 676;
Best Local Similarity 22.5%; Pred. No. 1.8;
Matches 102; Conservative 46; Mismatches 153; Indels 153; Gaps 24;

QY 295 TLQSWLLDAPCSLPAEALCWAPGGD-----PCQPLVPL--SWENVTVDK 339
DB 295 TLQSWLLDAPCSLPAEALCWAPGGD-----PCQPLVPL--SWENVTVDK 339

Db 130 TLRTTLLDFAHLVA---CF-APGGSPSSFPKYIDWLTCLGLVPIILKKRQEGVYTG 184
Qy 340 VLEFPPLKHPNLCVQVNSEKIQLOECLWADSLGPKLKDVLLETRGPONDRSLCALEP 399
Db 185 LRAF--LKQHP-----LTRLATVAEA-----AERAGPGFFELALAFD- 220
Qy 400 SGCTSLPSKASTRAA-----RLGEYLLQDL---QSGCQLWDDDLGALW---- 441
Db 221 -----STRVADYDRVYIYNHRRGDMVLRDPTSGGRCGLVLP-----PLMTGDR 266
Qy 442 -----AC-PMDKYIHKRWALVWLACLLFAAALSILLKKDHAKAAAGR 485
Db 267 LVFDSVPQRLFEIVACHSLREAH-----VCLRNTASVKVLLGRKSDSERGVAGA 318
Qy 486 AALL--LYSADSGFRLVAGALSCQLPLRVAVDLWLSRRELSAQGPVAMFHAQRQTL 543
Db 319 ARVANKVLGEDD---ETKAGSAASRL---VRLIINKGMRH-----VGDINDTVRSYL 365
Qy 544 QSGVVVLLFSPGAVALCSEWLQDVGSGCAHGPDAFRASLSCLVLPDFLOGRPGSVYG 603
Db 366 DEAG-----GHL-----IDAPAVDG-----TLPGF--GKGNSRGS 394
Qy 604 ACDFRLLHPDAVPALFRTPVFTPLSPDLF---GALQOPRAPRSG---RLQERAEQV 656
Db 395 AQODGGGRAPQLQARFTAVVNNINGVLEGIYINLFTGRIERTNAGLATQLQERDREL 454
Qy 657 SRALQALDYSFHPFCTPAGRGVSGPGAGD 690
Db 455 RRATAGALERQOQRAADLAAESVTGGCGSRPAGAD 488

RESULT 12
W70T_MOUSE STANDARD; PRT; 922 AA.
AC Q9D2V7:
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 70 kDa WD-repeat tumor rejection antigen homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
CC -1- SIMILARITY: BELONGS TO THE CORONIN FAMILY OF WD-REPEAT PROTEINS.
CC
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CC
DR EMBL; AK018739; BAB31380.1; -
DR MGD; MGI:1926135; 0610011B16rik.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 6.
DR PRINTS; PR003320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 2.
DR SMART; SM00320; WD40; 6.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS0082; WD_REPEATS_2; 4.
DR PROSITE; PS0294; WD_REPEATS_REGION; 2.
KW Repeat; WD repeat.
FT REPEAT 75 115 WD 1.
FT REPEAT 124 163 WD 2.
FT REPEAT 166 205 WD 3.
FT REPEAT 209 253 WD 4.
FT REPEAT 253 581 WD 5.
FT REPEAT 589 629 WD 6.
FT REPEAT 632 671 WD 7.
FT REPEAT 725 765 WD 8.
SQ SEQUENCE 922 AA; 100860 MW; C8E4BC1EB9CFE242 CRC64;

Query Match 2.7%; Score 102; DB 1; Length 922;
Best Local Similarity 21.1%; Pred. No. 3.6; Indels 254; Gaps 38;
Matches 146; Conservative 65; Mismatches 227;
Qy 130 QAYPTARCVLL-EGVQPAALVQFGVSGVYDYDCEFAALGSEVRIWYSY--OPRYEKELN 186
Db 112 EALSPVGVVLPBELPVEVLFQFHTVDCVLV----STAGTKVQVMDVAKQPLTELEA- 166
Qy 187 HTQQLPALPWLNVNSADGNVHLV-----NYSEEHFGLSLYW---- 224
Db 167 HKDLVQSAVW---SRDGAIVGTACKDKQLRIFDPRARTQASOSTQAHENNRDLAWTGI 223
Qy 225 -----NQVQPPKPRWHKNLTGPQI--ITLHNT--DLVPCL----- 256
Db 224 QEHLVSTGFNMREAREAKLMDTRLFSSALASYTLDTSPGLIPLDPSGLLVLAGKGN 283
Qy 257 ---CIQVWPLEPDSVTRTNCIFRE-----DPRAHQLWQAARLLTLQSWLL----- 301
Db 284 QLYCEVTPOQALSPVPTQCILENVLRGALVPRRALVMSCEVLOVLQSLTAIPISH 343
Qy 302 -----DAPCSLPAAALCWAPGDPQCPVLPPLSWENVTVDKVLEFPLL 346
Db 344 HVPRKAVEFHEDLPDPTAGSNPDAHMMWA--GD-----NQQVOKVSLNPAR 389
Qy 347 KGHENLCVQVNSSEKQLQOECLWAD---SLGPKDDVILLLE-----TRGPQDNRSIC 395
Db 390 RPHP-----CFTSLVPTMEPADVMPQPAEMPRADTDLSEGFSSPSL- 432
Qy 396 ALEPSGCTSL-PSKASTR--AARIGEYLLQDLSQCQLWDDDLGALWACPMKYIHKR 452
Db 433 -MSPSTSSLSSTSGICTSPSQRSLSLGSPC-----KFRHTQ 474
Qy 453 WALVWLACLLFAAALSILLKKDHAKAAAGRAALLYSADDSGFERLVGALASALCOL 512
Db 475 GS-----LHURSHITNLKG--LNLTPGESDGF-----CAN 504
Qy 513 PLRVAVDLWSRRELSAQGPVAMFHAQR-----RQLQEGGVVVL-----FSPCAVAL 560
Db 505 RLRVAVPL-----LSSGGEVAVLEQKRGRLPDTALPTLQNGTAVMDLVWDFDPHRLAV 559
Qy 561 CSEWLQDVGSGGANGHPDAFRASLSCLVLPDFLOG--RAPSIVYACFDRL-----LHPDA 614
Db 560 AGE-----DA-RIRLRVPPGGLNVLTPTTTLTGHTKIYSLRHFPLA 603
Qy 615 VPALFR-----TVPVFTLPSPDLFLGALQOPRAPRSCRQLQERAEQV--SRALQ----- 662
Db 604 ADVLASSYDLTVRIWDL-----QTGAERL-KLQGHQDQITFLAWSDPDGKOLA 650

Db	749	EDKLGQDKVKSIIELLRNAGIKIW-MLTGDKVETARC-----VSIKSLISRGQVYVHTIT--	801
Qy	162	CFEAALGSEVRWISYQTPRYEKELNHQOLPALPWLWNSA-----DGDNVHLVNLVNSEBQH	217
Db	802	-----KVTRP--EGAFNQLEVLK-----INRNACLLIDGESLGMFLKHYEQEF	842
Qy	218	EGLSYWNQV---QGPPKPNWH-----KNLTGPQIITL-----NHTDLVPCLCIQVW----	261
Db	843	FDVVVHLPTVIACRCTPOQKADVALVIRKMTGKRVCCIGDGGNDVSMIQACADVGVGIVGK	902
Qy	262	-----PLEPDSVRTNICPPREDDPRAHONLW-----QAARLRLLTQSLWLLDAPCSLPA	309
Db	903	EKGQASLAADFSTIQCHLTE-----LLLWHRGNSYKRSKAUQAQVMMRGLTIATCQ--A	955
Qy	310	EAALC-----WRAPGGDPCQPLVPPLPSWENVTVDKVLBLEPFLKLGHPNLCVQVNS	358
Db	956	VYSICSLFEPALYQGLWLVGATCYTMAPVFS---LTLDDHDIERSLTKIYPELYKELTE	1012
Qy	359	SEKL 362	
Db	1013	GKSL 1016	
RESULT 14			
UL06_HSVEB STANDARD; PRT; 753 AA.			
ID	UL06_HSVEB		
AC	P28944;		
DT	01-DEC-1992 (Rel. 24, Created)		
DT	01-DEC-1992 (Rel. 24, Last sequence update)		
DT	01-OCT-1996 (Rel. 34, Last annotation update)		
DE	Varion gene 56 protein.		
GN	56.		
OS	Equine herpesvirus type 1 (strain Ab4p) (EHV-1).		
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;		
OC	Alphaherpesvirinae; Varicellovirus.		
OX	NCBI_TaxID=31520;		
LN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=92295566; PubMed=1318606;		
RX	Telford E.A.R., Watson M.S., McBride K., Davison A.J.;		
RT	"The DNA sequence of equine herpesvirus-1.";		
RL	Virology 189:304-316(1992).		
CC	-!- FUNCTION: PRESUMED VIRION PROTEIN; POSSIBLE ROLE IN DNA		
CC	PACKAGING.		
CC	-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL6,		
CC	EHV-1 56, EBV BBF1, HCMV UL104, AND VZV 54.		
CC	-----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announ		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; M86664; AAB02491.1; -		
DR	PIR; B36801; WZBEE8.		
DR	InterPro; IPR002660; Herpes_UL6.		
DR	Pfam; PF01763; Herpes_UL6; 1.		
DR	ProDom; PD003210; Herpes_UL6; 1.		
SQ	SEQUENCE 753 AA; 83992 MW; C5E118F78BBED203 CRC64;		
Query Match 2.7%; Score 100.5; DB 1; Length 753;			
Best Local Similarity 22.98; Pred. No. 3.7;			
Matches 99; Conservative 46; Mismatches 190; Indels 97; Gaps			
Qy	295	TLQSLMLDAPCSLPAEAAALCWARGGDCQPLVPPLPSWENVTVDKVLBLEPFLKLGHPNLCV	354
Db	156	TLQSLMLDFVRSITA-----CFSASEPDGTASFAYIDW--IACLGILPIQLRKRAFGATV	209
Qy	355	QYNSEKILQLECLWADSLGPLKDDVLLLETRGPDNRSL-----CALE 398	


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Db 210 HPK -----LWR-----KLPTDVPSLES--CVDERDLAGKLYVANSLLREGLEAVVE 253
QY 399 PSQCT-SLPKASTRAARLGEYLLQDL-----OSQOCLQDWD---DDLGAALMACPMW 446
Db 254 LARCTASVAINMDYRNVIFHYTRREVAIDSTTTKRGCELVLMQIPWKDGSVLFDSPLQ 313
QY 447 KY-----IHKRWALVWLACILFAAALSLLILLKKDHAKAARGRAALLLYSADDSGFER 500
Db 314 RICEVCNCHALREHAKLQCLQNTVPVKILVGRKKDEAOGP--GWASKAVDKLMGEGEEL 371
QY 501 LVGALASALQCLPLRVAVDWSRRELSAQQGPVAFWFAORROTLOEGGVVVLFLSPCAVAL 560
Db 372 HSSSAASRL-----VKLVNKMMSRHIGDITETVRSYLNSTNLNSGAQVDTSLFG----- 423
QY 561 CSEWLQDVGSGPGAHGP-HDAFRASLSCVLPDFLOGRAPGSYVACFDRLLHPDPAVPALF 619
Db 424 ---FGSGKTKQGNMPPQEAFTSVINGMLEG-----YVN-----NLF 462
QY 620 RTVPVFTLPQLPDLGALQOPRAPRSGRQLQERAEQVSRALQPALDSYFHPGTPA--PG 677
Db 463 KTIEDLRTGNS-----GLLDQLR-DRESEITHLREQLLRVSQAADGSTQPGASSAALPG 516
QY 678 RGVPGGPGAG 689
Db 517 SGAKSGAG-GLG 527

RESULT 15
CLR3_HUMAN
AC Q9NYQ7: O75092; STANDARD; PRT; 3312 AA.
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Cadherin EGF LAG seven-pass G-type receptor 3 precursor (Flamingo
DE homolog 1) (hEmil) (Multiple epidermal growth factor-like domains 2)
DE (Epidermal growth factor-like 1).
GN CELSR3 OR CDHF11 OR FMIL OR EGF11 OR MEGF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20202599; PubMed=10716726;
RA Wu O., Maniatis T.
RT "Large exons encoding multiple ectodomains are a characteristic
RT feature of protocadherin genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
RN [2]
RP SEQUENCE OF 1954-3312 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98360089; PubMed=9693030;
RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
RT "Identification of high-molecular-weight proteins with multiple
RT EGF-like motifs by motif-trap screening.";
RL Genomics 51:27-34(1998).
CC -!- FUNCTION: Receptor that may have an important role in cell/cell
CC signaling during nervous system formation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.
CC -!- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 GPS DOMAIN.
CC
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CC -----
DR EMBL; AF231023; AAF61929.1; -
DR EMBL; AB011536; BAA32464.1; -
DR HSSP; P00740; 1EDM.
DR Genew; HGNC:3230; CELSR3.
DR MIM; 604264; -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF00028; cadherin; 9.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF01825; GPS; 1.
DR Pfam; PF02793; HRM; 1.
DR Pfam; PF00054; laminin_G; 2.
DR PRINTS; PR00205; CADHERIN.
DR PRINTS; PR00011; EGFLAMININ.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00112; CA; 8.
DR SMART; SM00180; EGF_Lam; 1.
DR SMART; SM00001; EGF_like; 6.
DR SMART; SM00303; GPS; 1.
DR SMART; SM00008; Hormr; 1.
DR SMART; SM00282; Lamg; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00232; CADHERIN_1; 7.
DR PROSITE; PS50268; CADHERIN_2; 8.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS0221; GPS; 1.
DR PROSITE; PS00449; G_PROTEIN_RECEP_F2_1; FALSE_NEG.
DR PROSITE; PS00850; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS50025; LAM_G_DOMAIN; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
KW Developmental protein; Hydroxylation; Signal.
FT SIGNAL 1 32
FT CHAIN 33 3312
FT CADHERIN EGF LAG SEVEN-PASS G-TYPE
FT RECEPTOR 3.
FT DOMAIN 33 2540
FT TRANSMEM 2541 2561
FT DOMAIN 2562 2572
FT TRANSMEM 2573 2593
FT DOMAIN 2594 2601
FT TRANSMEM 2602 2622
FT DOMAIN 2623 2643
FT TRANSMEM 2644 2664
FT DOMAIN 2665 2681
FT TRANSMEM 2682 2702
FT DOMAIN 2703 2725
FT TRANSMEM 2726 2746
FT DOMAIN 2747 2753
FT TRANSMEM 2754 2774
FT DOMAIN 2775 3312
FT DOMAIN 326 433
FT DOMAIN 434 545
FT DOMAIN 546 651
FT DOMAIN 652 756
FT DOMAIN 757 858
FT DOMAIN 859 961
FT DOMAIN 962 1067
FT DOMAIN 1068 1169
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FT DOMAIN 1170 1265 CADHERIN 9.
FT DOMAIN 1375 1433 EGF-LIKE 1, CALCIUM-BINDING.
FT DOMAIN 1435 1471 EGF-LIKE 2, CALCIUM-BINDING.
FT DOMAIN 1475 1514 EGF-LIKE 3, CALCIUM-BINDING.
FT DOMAIN 1515 1719 LAMININ G-LIKE 1.
FT DOMAIN 1722 1758 EGF-LIKE 4, CALCIUM-BINDING.
FT DOMAIN 1764 1944 LAMININ G-LIKE 2.
FT DOMAIN 1946 1982 EGF-LIKE 5, CALCIUM-BINDING.
FT DOMAIN 1983 2020 EGF-LIKE 6, CALCIUM-BINDING.
FT DOMAIN 2021 2053 EGF-LIKE 7, CALCIUM-BINDING.
FT DOMAIN 2055 2090 EGF-LIKE 8, CALCIUM-BINDING.
FT DOMAIN 2096 2131 LAMININ EGF-LIKE.
FT DOMAIN 2131 2158 GPS.
FT DOMAIN 2158 2477 BY SIMILARITY.
FT DISULFID 1379 1390 BY SIMILARITY.
FT DISULFID 1384 1421 BY SIMILARITY.
FT DISULFID 1423 1432 BY SIMILARITY.
FT DISULFID 1439 1450 BY SIMILARITY.
FT DISULFID 1444 1459 BY SIMILARITY.
FT DISULFID 1461 1470 BY SIMILARITY.
FT DISULFID 1479 1490 BY SIMILARITY.
FT DISULFID 1484 1500 BY SIMILARITY.
FT DISULFID 1502 1513 BY SIMILARITY.
FT DISULFID 1726 1737 BY SIMILARITY.
FT DISULFID 1731 1746 BY SIMILARITY.
FT DISULFID 1748 1757 BY SIMILARITY.
FT DISULFID 1950 1961 BY SIMILARITY.
FT DISULFID 1955 1970 BY SIMILARITY.
FT DISULFID 1972 1981 BY SIMILARITY.
FT DISULFID 1985 1996 BY SIMILARITY.
FT DISULFID 1990 2008 BY SIMILARITY.
FT DISULFID 2010 2019 BY SIMILARITY.
FT DISULFID 2019 2037 BY SIMILARITY.
FT DISULFID 2027 2040 BY SIMILARITY.
FT DISULFID 2042 2052 BY SIMILARITY.
FT DISULFID 2059 2074 BY SIMILARITY.
FT DISULFID 2061 2077 BY SIMILARITY.
FT DISULFID 2079 2089 BY SIMILARITY.
FT MOD_RES 1963 1963 HYDROXYLATION (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 847 847 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1182 1182 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1222 1222 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1317 1317 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1327 1327 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1649 1649 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1713 1713 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1770 1770 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2053 2053 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2177 2177 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2196 2196 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2386 2386 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2474 2474 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2506 2506 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 2158 2158 G -> GLRGAG (IN REF. 2).
SQ SEQUENCE 3312 AA; 358251 MW; BEC208703651A4A5 CRC64;
```

Query Match 2.7%; Score 100.5; DB 1; Length 3312;

Best Local Similarity 19.8%; Pred. No. 25;

Matches 190; Conservative 78; Mismatches 301; Indels 393; Gaps 47;

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Qy 26 GPQDATHSPGLSCRLWDS-DILPLGDIVPAPGPVLPAPTHQTELVLRCOKETDCDLC 83
Db 1953 GP-----CPHADCDRLQWTFCTCPG-----YGPCCVDACLINPCNQGSCR-- 1997
Qy 84 LRVAVHL--AVHGD-----HWEPDEKFGGAADSGVEPRNLSQ----- 122
Db 1998 -----HLPAGPHGYTDCVGGYFGHCHCEHMDQCPGRWWSFTCGPCNCDVHKGFDPNC 2052
Qy 123 -----AQVVLFSQAVP-----TAR-CVILEVQVPAALVQFGSVGS--- 157
Db 2053 NKTNGQCHCKEFHYRPRGSDSLPCDYPVGTSTSRSCAPHSGQCPCRPALGRQCNCSDS 2112
Qy 158 -----VVYD-----CFAALGSEVRINSYTPRYE 182
```

```
Db 2113 PPAEVTASGCRVLYDACPKSLRSGVWVPQTKFVLATVPCPRGALGAARVRLCDEAOGWLE 2172
Qy 183 KEL-NHTQOOLPALPWLNVNSADG-----DN----- 205
Db 2173 PDLFNCTSPAFRELSLLDGLLELNKKTALDTEAKKLAORLREVTGHTDHYFSQDVRVT 2230
Qy 206 ----VHLV-----LNVSEEQHFGLSLYWN-----VQGGPKPRWHKN 238
Db 2231 ARLLAHLAFESHQOGFGTATQDAHFENENLLWASALLAPETGDLWALGORAPGCGSPG 2290
Qy 239 LTG-----PQITLNLHTDLV-PCLCIQVWPLE-PDSVRTNICPFREDPRA 281
Db 2291 SAGLVRLHEEYAATLARNMELTYLNPMLGLVTPNIMLSIDRMEHPSPR---GARRYPRY 2346
Qy 282 HONLWQAARLLTLTQSWLLDAPCSLPAAALCWAPGDCQPLVPPLSWENVTVDKVL 341
Db 2347 HSNLFRGQ-----DAMDPTHVLLPSQ-----SPRSPSEVLPTSSSIENSTTSVV 2393
Qy 342 EFPL-LKGHPNLCVOVNSSEKILQOECLWADSLGPKDDVLLLETRG---PQD----- 390
Db 2394 PPPAPPEPEPGISIII-----LLVYRTLGLLPAQFOAERRGARLPQNPVMSV 2443
Qy 391 -----NRS---LCA-LEPSG-----CTSL 405
Db 2444 VSVAVFHGRNFRGLTESPISLEFRLLTANRKAICVQWDPPLGAEQHGVTARDCELV 2503
Qy 406 ---PSKASTRAARLGEY-LLODLQSGOCILQWDDDLGALWACPMOKYIHKRWALVLA 461
Db 2504 HRNGSHARCRCRTCTFGVMDASPRERL---EGDLELLAV-----FTHVVAVSVAALV 2555
Qy 462 LFAAALSILILLKKD---HAK-AAARGAALL----- 489
Db 2556 LTAAILLSLRSLKSNVRGIHANVAAALGVAELLLGTHRTNQLVCTAVAILHYFFLS 2615
Qy 490 -----LYSAD-----DSGFERLVGALASALCOLPLRVAVDL-----W 521
Db 2616 TFAMLFVQGLHLYRMQVEPRNVDRGAMRFYHALGWVPVAVLLGLVGLDDEGYGNPDFCW 2675
Qy 522 SRRELSAQGPVAMFHA-----ORRQ-----TLQEGGVVV 550
Db 2676 ---ISVHEPLIWSFAGPVVLVIVMGTMLAARTSCSTGOREAKKTSALTLSRSL 2731
Qy 551 LLFSP-----GAVALCSEWLQDQVSGPGAHGPHDAFRASLSCVLPDFLOGRAPS 606
Db 2732 LLVSASWLFGLLVNHSILAFHYLHAGLGLQGLAVLLIFCV---LNADARAAMPACL 2787
Qy 607 DRLLHPDAV-----PALFRTPVPVFTLPSQLPDFLGA---LOQPRAPSRGRLOERAEQVS 657
Db 2788 GRKAPEEARPAPGLGPGAYNNNTALFBSGLIRITLGASTVSSVSARSGRTOQDQSORG 2847
Qy 658 RA 659
Db 2848 RS 2849
```

Search completed: February 24, 2003, 09:21:56

Job time : 27 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 24, 2003, 09:21:27 ; Search time 41 Seconds
(without alignments)
3477.673 Million cell updates/sec

Title: US-09-608-918-2
Perfect score: 3716
Sequence: 1 MPVPWFLLSLALGRSPVLS.....TPAPRGVGVGAGPGAGDGT 692

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SP TREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mmc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2598	69.9	538	Q9BR97	Q9br97 homo sapien
2	1812.5	48.8	567	Q99J43	Q99j43 mus musculus
3	215	5.8	311	Q8R335	Q8r335 mus musculus
4	131.5	3.5	4340	O30764	O30764 streptomyc
5	131	3.5	482	O8TEC2	O8tec2 homo sapien
6	130.5	3.5	1366	Q92529	Q92529 streptomyc
7	116.5	3.1	1665	Q8V111	Q8v111 mus musculus
8	116	3.1	1021	Q96M86	Q96m86 homo sapien
9	115.5	3.1	745	Q8XED7	Q8xed7 escherichia
10	114.5	3.1	745	Q9EYF6	Q9eyf6 escherichia
11	114.5	3.1	1193	Q9HZES	Q9hze5 pseudomonas
12	112.5	3.0	657	Q96DW2	Q96dw2 homo sapien
13	112.5	3.0	744	Q96F55	Q96f55 homo sapien
14	111.5	3.0	405	O8TZU1	O8tzu1 pyrococcus
15	111.5	3.0	478	Q9RY89	Q9ry89 deinococcus
16	111	3.0	1279	Q66031	Q66031 cercopithec

17	110	3.0	757	6	Q9N015	Q9n015 macaca fasc
18	109.5	2.9	620	4	Q9HCN6	Q9hcn6 homo sapien
19	109	2.9	427	2	Q9S116	Q9s116 streptococ
20	109	2.9	603	12	P89140	P89140 pseudorabie
21	109	2.9	604	12	Q9YVB7	Q9yvb7 pseudorabie
22	109	2.9	1343	12	Q06635	Q06635 bovine herp
23	108.5	2.9	1072	4	Q96EP0	Q96ep0 homo sapien
24	108	2.9	361	2	O86410	O86440 pseudomonas
25	108	2.9	2629	11	P97499	P97499 mus musculu
26	108	2.9	10917	2	Q93NW6	Q93nw6 streptomyc
27	107	2.9	719	16	O69992	O69992 streptomyc
28	107	2.9	1001	16	Q9K2M8	Q9kzm8 streptomyc
29	107	2.9	1118	4	Q15426	Q15426 homo sapien
30	107	2.9	4928	2	Q9ALM3	Q9alm3 saccharopol
31	106.5	2.9	679	16	Q9F2P6	Q9f2p6 streptomyc
32	106	2.9	1211	11	Q9ROL3	Q9rol3 rattus norv
33	106	2.9	1235	11	Q9ROL5	Q9rol5 rattus norv
34	106	2.9	1273	11	Q9ROL4	Q9rol4 rattus norv
35	106	2.9	1531	5	Q9W0P8	Q9w0p8 drosophila
36	106	2.9	9510	2	Q93NX9	Q93nx9 streptomyc
37	105.5	2.8	1354	11	Q9EPW8	Q9epw8 mus musculu
38	105.5	2.8	1542	4	O15035	O15035 homo sapien
39	105	2.8	1766	12	Q9J599	Q9j599 fowlpox vir
40	104.5	2.8	277	16	O53500	O53500 mycobacteri
41	104	2.8	1256	11	Q99W76	Q99w76 rattus norv
42	104	2.8	1487	5	O15843	O15843 leishmania
43	103.5	2.8	828	16	Q8ZBL4	Q8zbl4 yersinia pe
44	103.5	2.8	2055	4	O75055	O75055 homo sapien
45	103	2.8	384	4	Q8TDX1	Q8tdx1 homo sapien

ALIGNMENTS

RESULT 1

Q9BR97 PRELIMINARY; PRT; 538 AA.
AC Q9BR97;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Hypothetical 59.1 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006411; AAH06411.1;
KW Hypothetical protein.
SQ SEQUENCE 538 AA; 59127 MW; 65B6344DA6A5AFD2 CRC64;

Query Match 69.9%; Score 2598; DB 4; Length 538;
Best Local Similarity 99.4%; Pred. No. 6.1e-207;
Matches 480; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MPVPWFLLSLALGRSPVLSLRLVLPQDATHCSPGLSCLRLWDSILCLPGDIVPAGPV	60
Db	1	MPVPWFLLSLALGRSPVLSLRLVLPQDATHCSPGLSCLRLWDSILCLPGDIVPAGPV	60
Qy	61	LAPTHLOQLVLRCKETDCDCLRVAVHLAVHGWPEDEEKGGAADSGVEEPNRS	120
Db	61	LAPTHLOQLVLRCKETDCDCLRVAVHLAVHGWPEDEEKGGAADSGVEEPNRS	120
Qy	121	LQAVQLSFQAYPTARCVLLEQVPAALVQFGQSVGVYDCFEALGSEVRWISYTPQR	180
Db	121	LQAVQLSFQAYPTARCVLLEQVPAALVQFGQSVGVYDCFEALGSEVRWISYTPQR	180
Qy	181	YEKELNHTQQLPALPWLNVSDGONVHLVNVSEQHFGLSLYMNQVQGPCKPRHKNLT	240
Db	181	YEKELNHTQQLPALPWLNVSDGONVHLVNVSEQHFGLSLYMNQVQGPCKPRHKNLT	240

Db 181 YEKELNHTQOLPALPWLNVNSADGDNVHLVNLVNSEQHFGSLYVNOVQGPCKPRHKKLNT 240
QY 241 GPQIITLNTDLVPCICIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLLTLTQSWL 300
Db 241 GPQIITLNTDLVPCICIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLLTLTQSWL 300
QY 301 LDAPCSLPAEALCWAPGDCQCPVLPPLSWENVTVDKVLFFLLKGHPNLCVQVNSSE 360
Db 301 LDAPCSLPAEALCWAPGDCQCPVLPPLSWENVTVDKVLFFLLKGHPNLCVQVNSSE 360
QY 361 KIQLOECLWADSLGPKLDDVLLLETRGPQDNRSICALPEPSCSTSLPSKASTRAARLGEYL 420
Db 361 KIQLOECLWADSLGPKLDDVLLLETRGPQDNRSICALPEPSCSTSLPSKASTRAARLGEYL 420
QY 421 LODSQGQCILQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLIILLKKDHAKA 480
Db 421 LODSQGQCILQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLIILLKKDHAKA 480
QY 481 AAR 483
Db 481 WLR 483

RESULT 2
Q99J43
ID Q99J43 PRELIMINARY; PRT; 567 AA.
AC Q99J43;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE Hypothetical 62.8 kDa protein.
GN IL17RL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004759; AAH04759.1; -.
DR MGD; MGI:2159336; IL17rl.
KW Hypothetical protein.
SQ SEQUENCE 567 AA; 62798 MW; C1AAAB79E2006B1D CRC64;

Query Match 48.8%; Score 1812.5; DB 11; Length 567;
Best Local Similarity 62.9%; Pred. No. 8.8e-142;
Matches 357; Conservative 50; Mismatches 130; Indels 31; Gaps 7;

QY 1 MPVPWFLLSLALGRSPVLSLERLVGPQDATHCSPLGSLCRLWDSIDLCLPGDIVPAGCPV 60
Db 1 MPVSWFLLSLALGRNPVVSLERLMEPDQTARCSLGLSCHLWDGDLVLCPLGSLQSAFCPV 60
QY 61 LAPTHLQTELVLRCOKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVBEPRNAS 120
Db 61 LVPTRLQTELVLRCOKETDCALCVRVVHLAVHGHWAPEE----AKGSDSELESRNAS 116
QY 121 LQAQVYLSFQAYPTARCVLLEVOVPAALVOFGSGSVVYDCFPAAALGSEVIRINSYTPR 180
Db 117 LQAQVYLSFQAYPIARCALLLEVQVADLVQPGSGSAVDFCFEASLGAEVQINSYTKPR 176
QY 181 YEKELNHTQOLP-----ALPWLNVNSADGDNVHLVNLVNSEQHFGSLYVNW 225
Db 177 YEKELNHTQOLPDCRGLEVRDSTQSCWVLPWLNVSTDGDVNLTLTLDVSEEDQFSFLYLRL 236
QY 226 YQGGPKPRWHKNTLGPQIITLNTDLVPCICIQVWPLEPDSVRTNICPFREDPRAHONL 285
Db 237 PVPDALKSLWYKNTLGPQIITLNTDLVPCICIQVWPLEPDSERVECPFPREDPCAHRNL 296
QY 286 WQAARLLTLTQSWLIDAPCSLPAEALCWAPGDCQCPVLPPLSWENVTVDKVLFFLL 345
Db 297 WHIARLRLVSPGWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPVPQKNATVNEPQDFQL 356

QY 346 LKHPNLCVQVNSSEKLOECLWADSLGPKLDDVLLLETRGPQDNRSICALPEPSCSTSL 405
Db 357 VAGHPNLCVQVNSSEKLOECLWADSLGPKLDDVLLLETRGPQDNRSICALPEPSCSTSL 416
QY 406 PSKASTRAARLGEYLLODLSQGQCILQWDDDLGALWACPMCKYIHKRWALVWLACLLFA 464
Db 417 PSMASTRAARLGEYLLODLSQGQCILQWDDDLGALWACPMCKYIHKRWALVWLACLLFA 476
QY 465 AALSLLIILLKKDHAKAARAAALLLIY-----ADDSGFERLVGLASALCOLPLRVAV 518
Db 477 AALFFELLKLDKDMTPSPPGSAACYPIACKAGRPAAATSG-STSGCCTCTLC--PPRSAS 533
QY 519 DLWSRRELQAQGPVAFWFAHQRTQTQEG 546
Db 534 PRSSPCPSR--LSWMHCREAAPLPRG 559

RESULT 3
Q8R335
ID Q8R335 PRELIMINARY; PRT; 311 AA.
AC Q8R335;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Hypothetical 34.1 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026737; AAH26737.1; -.
KW Hypothetical protein.
SQ SEQUENCE 311 AA; 34102 MW; 00E706D6617CFF15 CRC64;

Query Match 5.8%; Score 215; DB 11; Length 311;
Best Local Similarity 29.0%; Pred. No. 1.1e-09;
Matches 81; Conservative 33; Mismatches 117; Indels 48; Gaps 10;

QY 418 EYLLQDLQSGQCILQWDDDLGALW---ACPMCKYIHKRWALVWLACLLFAAALSLI-L 473
Db 53 DLIIPFLQENCILVRSVDQFANKHVLCP--DVSHRHGLGLLILALLALTALVGVVLVLL 110
QY 474 KDHAKAARAAALLLYSADDSGFERLVGLASALCQLPLRVA-----VDLMSRRE 525
Db 111 GRRLPLGSGRTPVLLHHAADSEAORRLVGAEL-----LRTALGGGRDVIWDLWEGTH 165
QY 526 LSAQGPVAFWFAHQRTQTQEGVGVVLLFSPGAVLCSLWQDGVSGPGARHPDAFRASL 585
Db 166 VARIQPLPWLWAAREVAREQGTVLLLNW-----CAGPSTACSGDPQAASL 211
QY 586 SCVLPDFLQGRAPGVSYGACFDRLHPDAVPALFRTVPVFTLPSQLPDFLQALQ-OPRAP 644
Db 212 RTLL-----CAAPRLLLAYFSLCAKGDIPRLPALPRYRLRLDLRLRALDAQPATL 266
QY 645 RSG-----RLQERAEQVS-RALQPALDYSFHPPGTP 674
Db 267 ASSWSHLGAKRCKLNKEQCHLELEAAKDDYQGSTNSP 305

RESULT 4
O30764
ID O30764 PRELIMINARY; PRT; 4340 AA.
AC O30764;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE Polyketide synthase modules 1 and 2.
GN NIDAL.
OS Streptomyces caelestis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

```
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=36816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL-2821;
RX MEDLINE=98053867; PubMed=9393718;
RA Kakavas S.J., Katz L., Stassi D.;
RT "Identification and characterization of the niddamycin polyketide
  synthase genes from Streptomyces caelestis.";
RL J. Bacteriol. 179:7515-7522(1997).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
  (SDR) FAMILY.
CC EMBL; AF016585; AAC46024.1; -.
DR InterPro; IPR002106; AatRNA_ligaseII.
DR InterPro; IPR001227; AC_transferase.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR004410; Fadh.
DR InterPro; IPR000794; Ketoacyl-synt.
DR InterPro; IPR003880; Ppanthe_attach.
DR Pfam; PF00698; Acyl_transf; 3.
DR Pfam; PF00106; adh_short; 2.
DR Pfam; PF00109; ketoacyl-synt; 3.
DR Pfam; PF02801; ketoacyl-synt C; 3.
DR Pfam; PF00550; pp-binding; 3.
DR TIGRFAMs; TIGR00128; fadh; 3.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN1.
DR PROSITE; PS00075; ACP_DOMAIN; 3.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 2.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN1.
KW Oxidoreductase; Phosphopantetheine; Transferase.
SQ SEQUENCE 4340 AA; 457589 MW; D59A734CB5FB795D CRC64;

Query Match 3.5%; Score 131.5; DB 2; Length 4340;
Best Local Similarity 21.5%; Pred. No. 0.3;
Matches 146; Conservative 60; Mismatches 225; Indels 247; Gaps 30;

QY 168 GSEVRIWSTQRYEKELNHTQOLPALPNVNSADGNVHLVNLVNSEQHFGLSLYNQV 227
DB 1692 GPRTALEETAQHLHQGIRHT-----WLKVS-----HAFHSALMDPM 1728

QY 228 QG-----PPKRWKHLNHTQITLNLHTDLVPCLCIQVWPLE-----PDS 267
DB 1729 LGAFRDTLNLVQPTPLISNLTG-QIADPNH-----LCTPDYWIHARHTVREFA 1781

QY 268 VRTNICPFREDPAHONLWQAARLLTLQSWLLDAPCSLPA-----EALCWR 316
DB 1782 VQT-----AHDQRTTYLEIGAHTPLTLLHHTLDNPTTPTLHREHPETLTATL 1836

QY 317 APGGD-----PCQPLVPLSW-ENVTVDKVLEFPLKLGHPNLVCQVNSS 359
DB 1837 HTTGHTTTLHTTSPQTHLDTPTPFQDRYMWEPVRVAQV-----SGQP-----GA 1883

QY 360 EKLOLQ-----ECLWADSLGLPKDDVLLLETRGPQDNRLCALE-----P 399
DB 1884 DRLRYRVVNEAAPEHTVPSAERWLLLGSDPADAGILVGEVEQLVGHGAAVQRLDIPAP 1943

QY 400 SG-----CTSPSKAST-----RAARLGE-YLLQDL-QSQCLQLWDDDLGAL 440
DB 1944 AGRRLLPSCSELPVRGSHTGFECSRSLRSPRVAEAVALLQALGDGADAPLMIATRGAV 2003

QY 441 WACPMKDYI-----HKKRWLVWLACLLFAAALSLLTLKDKHAKAAAGRAALLYSADDSG 497
DB 2004 AAAGEAFSVGGAQLMGLQVAGLELADRWGGLVLDLPADPAPALRGLARVLVSNAPDN- 2062

QY 498 FERLVGALASALCQLPLRVAVDLSRRELISAQG-PVAMFHAORROTLOEGGVVLLFSPG 556
DB 2063 -----QVAIR-ASGVFVRVVPAPCRPVR-----2085

QY 557 AVALCSEWLQD-----VSGPGAHGHDFAFRSLSCVLPDLQGRAPGSVYGACFDRL--- 609
DB 2086 -----NDWAPSGTVLTIGTGTGALGSOVARRLALAGAPHILLLAGRRGNSGAAELVDEL 2140

QY 610 -----LHPDAVPALFRTVPVF-----TLPSQLPDFLGAQQPR 642
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DB 2141 GAETVVAACDAARDALVLSLATIPEHRPLTAVLHAAGVLDGGLTPTERIDAVLRK 2200
QY 643 APRSGRLQERAEQVS-----RALQPALDSYFHPGTPAPGRGV 680
DB 2201 ATAARHLDLTDADLDLDAFVLFSSIVGVWGNGOATYAAANAALDALAH--GRRARGQA 2258
QY 681 -----GPGAGPG--AGDG 691
DB 2259 TSIANGPWAGSGMAAGDG 2276

RESULT 5
Q8TEC2 PRELIMINARY; PRT; 482 AA.
AC Q8TEC2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CDNA FLJ23658 fis, clone COLF3416.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON MUCOSA;
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074238; BAB85028.1; -.
SQ SEQUENCE 482 AA; 54139 MW; 4164B5A73026B385 CRC64;

Query Match 3.5%; Score 131; DB 4; Length 482;
Best Local Similarity 31.7%; Pred. No. 0.018;
Matches 45; Conservative 18; Mismatches 45; Indels 34; Gaps 7;

QY 237 KNLTPGQIITLNLHTDLVPCLCIQVWPLEPSDVRTNITCFREDPPRAH-QNLWQAAR----- 290
DB 223 KIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPFQSWPEAYGSDFKSVHFTDYS 282

QY 291 -----LRLTLQSWLLDAPCSLPAEALCWAPGGPCQPLVPLSWENVTVDK-----V 340
DB 283 QHTQVMVMAITLR-----CPLKLEAALCQRHDWHTLCKDL-----PNATARES DGWYV 329
QY 341 LEFPLKLGHPNLVCQV-----NSS 359
DB 330 LEKVDL--HPQLCFKFSFGNSS 349

RESULT 6
Q9Z529 PRELIMINARY; PRT; 1366 AA.
AC Q9Z529;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative large Pro/Ala/Gly-rich protein.
GN SC05710 OR SC9F2.06C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Murphy L., Harris D.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
```

RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL035559; CAB37473.1;
 SQ SEQUENCE 1366 AA; 141042 MW; FB954569D87D029B CRC64;

Query Match 3.5%; Score 130.5; DB 16; Length 1366;
 Best Local Similarity 22.4%; Pred. No. 0.079;
 Matches 175; Conservative 57; Mismatches 238; Indels 311; Gaps 42;

QY 21 LERLVGPDAHCSPGLSCLRLWDSILPLGDIVPAGPVLPATHLQTEVLVLCQKQETDC 80
 DB 675 LGALADPDAGH--PLTIRLLSEVRAALPGP--PAPVPTVRDAVETAYLDL----- 721

QY 81 DLCLRVAVLHVHGWPEDEKEFGGAA-----DSGVPEPRNASL-QAQQVLSFOA 131
 DB 722 -MCLRVATRLA-----DENGRLGTAVRLIAKVSQVHEAARRSLGPGGGGLDRES 771

QY 132 YPT-----ARCVLLE-VQVPAAL-----VOFGOSVG 156
 DB 772 FETLPPCGPAPARLGGGTGWAPAVLAEGLVFTGSGYRFAHELAEDWIOGTHLDLEALR 831

QY 157 SVVYDCFAALGSEVRINSYQTPRYKEKELNHTQQPALPWLNVSDGDNVHLVNSYEQ 216
 DB 832 ALVHR-RDTPLGT-----HRTTLP-VPHHRI--GSVVEALLLLA-RQ 868

QY 217 HFGLSLVYNQVGGPKPRWHKNTLGPQIITLNHTDLVPCLCIQVWPLEPDSVNTNCPFR 276
 DB 869 H-----GVQ-----LAUTLELVHAL-----D 886

QY 277 EDPRAHQNLMOAARLLTLQSLWLDAPCSLPAEAL-----CWAPGPGPCQPLVPP 329
 DB 887 RDPHS-----MWAARL-----LAEALTRVDPATYTDVLRLLADGIAERAGDQPTQVFGP 938

QY 330 LSWENVYDKVLEFPFLKGNHNLVQVNSSEKLOECLWADSLGPLKDDVLLLETRGPQ 389
 DB 939 AFTAPRVPAATRLDLR-----RLVLAD-----GPP 965

QY 390 DNRSILCALEPGCTSLPSKASTRAARLGEYLLQDLQSGCQLQ-LWDDDLGALWACPMOKY 448
 DB 966 H-----EFG-----PHLDTAAG-----LLVADPTVQPLLRVWFDDERPLPATP----- 1005

QY 449 IHKRWALVWLACLLFAAALSILLKKDHAKAAAGRAAL-----LLYSADD 495
 DB 1006 -----HATVATAQAALLHTRHRLDGLTEVLVDSTH 1037

QY 496 SGRERLVGALA-----SALCOLPLRVAVDLWSRRELSAOGPVAFWHAQRR-----QT 542
 DB 1038 RRADELLAVLAEEPSALCR-----AVERWARDERPARHRAAVTHGLRTAPHARSGADRT 1092

QY 543 LOEGGVVLLFSP-----GAVALCSEWLQDGVSGGAHGP-----DAFRA----- 583
 DB 1093 LRLHAALVLLAGPSDPLRGGALL-----VQDPCRHLPAALDLFAACDYLPP 1145

QY 584 LSLSCVLPDFLOGRAPSGVYGACFDRLHLPDAVPALFR-----TVPVFTLPSQDPLFGAL 638
 DB 1146 SAVAAALPTH-----PEPVLEAFARLLGPDAGEALLRLADATTALT--HRVAALVGR 1198

QY 639 QQPAPRGRGRLOERAQVSRAL--QPALDSYFHPPT-----PAPGRGVGPGAGPGAGD 690
 DB 1199 VTERPETAGHL---AAYVDRRLDRDPAPRAVLLPLVTRLLDDGPEPARAA--LAGVLAAD 1253

QY 691 G 691
 DB 1254 G 1254

RESULT 7
 Q8VIII ID Q8VIII PRELIMINARY; PRT; 1665 AA.
 AC Q8VIII;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE PDZ-domain protein scribble.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=CEREBELLUM;
 RA Mattock K.L., Kurschner C.;
 RT "Molecular cloning of mouse Scribble cDNA";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF441233; AAL32469.1;
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003591; LRR_typ.
 DR Pfam; PF00560; LRR; 13.
 DR Pfam; PF00595; PDZ; 4.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00369; LRR_TYP; 13.
 DR SMART; SM00228; PDZ; 4.
 DR PROSITE; PS0106; PDZ; 4.
 SQ SEQUENCE 1665 AA; 179749 MW; BE1272F4ECBF010E CRC64;

Query Match 3.1%; Score 116.5; DB 11; Length 1665;
 Best Local Similarity 23.5%; Pred. No. 1.5;
 Matches 140; Conservative 49; Mismatches 241; Indels 167; Gaps 30;

QY 126 VLSEFQAYPTARCVLLEQVPAALVQFGSVGSVYDCEFAALGSEVRINWSTQ----- 178
 DB 1172 VLVDGDEDTSTTAALEVS-----PGVIANPFAAGLHGRNSLESISDRELSP 1219

QY 179 --PRYKEKELNHTQOLPALPWLNVSD--GDNVHLVNLVNSEQHFGLSLVYNQVGGPKPR 234
 DB 1220 EGPGEKEL---ASQALPWESESAETTGRLNLE-----PLKLDYRALAALPSAG 1264

QY 235 WHKNLTGPGQIITLNHTDLVPCLCIQVWPLEPDSVNTNCPREDPRAHQNLWQAARLL 294
 DB 1265 SLQR--GPSATTGKTTAEP-----SPGSGQTK-----PGVIQPLAQA----- 1301

QY 295 TLQSWLLDAPCSLPAEALCWRAPGPGPCQPLVPPLSWENY--TVDKVLEFPLKGNHNL 352
 DB 1302 ---W-----PRNSPAP-----RGRGG--PCSPSPDELPAVNVKQAYRAFAAVPTVHPENS 1347

QY 353 CVQ-----VNSSEKLOECLWADSLGPLKDDVLLLETRGPQDNRSILCALEPGCTSLP 406
 DB 1348 ATQPTPGPAASPEQSLFRE-----RQYFELEVRVQAGPPKRVSLVGADDLR 1397

QY 407 SKASTRAARLGEYLLQDLQSGCQLQWLDDDLGALWACPMOKY-IHKRWALVWLACLLFAA 465

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Db 1398 KMOEEARKLQKRAQMLREEAVTSGPDMGLASDRSPDDQOEAEPWAV----- 1447
Qy 466 ALSLIILLKKDKHAKAA-----RGAALLLYSADSGFRELVCALASALCQLPLRVAV 518
Db 1448 -----PSHAGSGSPSPPLGGNAPVTKAERRHQERL--RMQSPELPAPER-AL 1495
Qy 519 DLWSRRELSAAGPVMFHAORROTLOEGGVVLLFSPCAVALCSEWLODVGSGPGAHGPH 578
Db 1496 SPERRALEAKRALM--RAARMKSLQODALRAQMV-----LSKSQEGRGKRGPL 1543
Qy 579 DAFRASLS-----CVLPDF-LQ-----GRAPGYVGACFDRLLHDPDAVPALFRTVPVF 625
Db 1544 ERLAEPSPAPTSPPTPLEDFGLTSPGRLPLS--GKFDY-----RAFAALPSSRRVY 1597
Qy 626 TLPSQLPDFLQALQOPRPSGRQLQRAEQVSRALQPALDSYFHPGTPAPGRGVGP 682
Db 1598 DI--QSPDFVEELRTLEASPSGQEBGEVALVLL-----GRPSPG-AVGP 1641

RESULT 8
Q96M86
ID Q96M86 PRELIMINARY; PRT; 1021 AA.
AC Q96M86;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE CDNA FLJ32752 fis, clone TESTI2001661, weakly similar to dynein beta
DE chain, flagellar outer ARM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RT NEDO human cDNA sequencing project.
RL EMBL; AK057314; BAB1423.1;
DR InterPro; IPR004273; Dynein_heavy.
DR Pfam; PF03028; Dynein_heavy; 1.
SQ SEQUENCE 1021 AA; 112942 MW; A1207BD978EA4D0D CRC64;

Query Match 3.1%; Score 116; DB 4; Length 1021;
Best Local Similarity 24.0%; Pred No. 0.86;
Matches 183; Conservative 75; Mismatches 276; Indels 228; Gaps 44;

Qy 55 PAPGVPVLAPTHLOTLEVLRCQKEDDCLRVAVHLAVHGWEEPEDEERFGGAADSGVE 114
Db 294 PAPGPGPEPLSLQKLILWRVLRPE---CLAGALADFTTSLGRPLDENTY---ATMPF 347
Qy 115 EPRNASLAQVVLVSOQVPTARC-VLLEVOVPAALVQFQSGVSVYDCFEALGSE--- 170
Db 348 KHSQATQPMILLPPGPHSATLHLPTVTQKLAAYQOQKQLQVI-----ALGSEAWD 401
Qy 171 ---VRISYTPRYEKELNHTQOLPALPWLNVSDGDNVHLVNLVSEEHFGLSLWNQV 227
Db 402 PVSVVVSTLSQAMYE---GH-----WLVL-----DNCHLM----- 428
Qy 228 OGPKPRWHKLTGQIITLNHTDLVPCICIQWPLEPSVTRNTPCFREDPRAHQNLW- 286
Db 429 -----PHWPKELLQLLELGRKAVVADLESQLLDOPES--RNVSTVHRDFR----LWL 477
Qy 287 -----QAARLRLTLQS-----W-----LLDAPCSLPAEALCWRAPGSDQCPV 327
Db 478 IVPRESSASLPAVLTHQSMFVFNQSLGLGHVLID---SVELAQQVLYWQP---PTQAL- 530
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Qy 328 PPLSWENVTVDKVLEPPLLKHPNLCVQVNSSEKILQLECLWADSL----- 373
Db 531 PLLLLHGLLHRLQYCYTRLQAHGRMSQVTLTVQVLTQDQOLMA-SLSNPRAAMQELAASV 589
Qy 374 ---GPKLD-----DVLLETRG-----PDNRSICA-LEP-----SGCTS 404
Db 590 FYGGPLGDTEDREALISLTQACLSPSSGSGVWPQHTPQSLIATLMLPELRELDMAECKA 649
Qy 405 ---LPSKASTAARLGE-----YLLQDLSGOCLOLWDDDLGALWACPMKY 448
Db 650 QMHLPSPPPEPLCGUSEGPAWLRRQSRALLSALQSRSPVWVPSRRGAQLA---ERR 706
Qy 449 IHKRWALVLAQLLFAAALSLLILLKKDHAKA-----AARGRAALLYSADSGFER 500
Db 707 LRQR--LVQVNRRESLQDLTHVIRQDESADPWSVLGPNARRPLEGVLETEALE--LSQ 762
Qy 501 LVGALASAL-COL-----PLR-----VAVDLMSRR-----ELSAQGPVAMFHA 537
Db 763 LVGTLLQRLDCLLQQLKGAPPCPSRRCAAVAHALMTGRLPLPWRPHAPAGPQPPNHWL-- 820
Qy 538 QRRQTLQEGVVVLLFSPCAVALCSEWLODVGSGPGAHGPH-DAFRASLSCLVLPDFLQGR 596
Db 821 --RQLSRRGQLLVRYLGVA-----DASSDVPERVHFILSAFRHRRLLLA--LRGE 867
Qy 597 A-----PGSVYGACFDRL---LHPDAVPALFRTV--PVFTLPQO--LPDFLGA 637
Db 868 RALDONVSSNFPFGRS-GSVSQQLQYKRLMNSNPLHFRVGNPNPTVPERGLLLIGLOV 926
Qy 638 LQOPRAPSRLQRAEQVSRALQPALDSYFHPGTP---PAP 676
Db 927 LHAEDPIAGALQDSSPSPQSPPLPVSIS-TQAPGTSDLAP 967

RESULT 9
Q8XED7
ID Q8XED7 PRELIMINARY; PRT; 745 AA.
AC Q8XED7;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE YehQ protein.
OS Escherichia coli O157:H7.
GN YEHQ OR Z3295 OR ECS2931.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Fen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT *Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.;
RL Nature 409:529-533 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT *Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.*;
RL DNA Res. 8:11-22 (2001).
DR EMBL; AE005439; AAC57188.1;
DR EMBL; AP002560; BAB36354.1;
KW Complete proteome.
```

```
FT CONFLICT 704 704 H -> Y (IN REF. 2).
SQ SEQUENCE 745 AA; 82593 MM; 37F8C754DE811F43 CRC64;

Query Match
Best Local Similarity 3.1%; Score 115.5; DB 16; Length 745;
Matches 162; Conservative 70; Mismatches 234; Indels 291; Gaps 43;

QY 21 LERLVGPQDATH-----CSPGLSCLRWSDIILCLPGDIVPAGPVLAPHTLQTELVLRC 74
DB 110 LEELATLPDTRKRAQVLVAKGTTIELF-----CAPGEIPSARLP-MSDVFYSSRSIRF 163
QY 75 QKETDC---DCLRVAVHLAVHGHWEPEDEKFF-----GAADSGVEEPRNA 119
DB 164 AR-CDCEITGLCEHV--LAVQAFVEAKTQQAETHLIWQMRSEHVTSSDDPFASEEGNA 220
QY 120 SIQ-----AOWVLSFOA-----YPTARCVLLEVOVPAALVQFGSGVSV 159
DB 221 CRQYVQOLSOALWLGISQPLIHAEAFSRAQQAERCNWR--WVSESLRQLRASV--- 274
QY 160 YDCEFAA-----LGSEVRIWSTQPRYKELNHTQOL-----PALPWLNVYADG-- 203
DB 275 -DAFHARASHYHAGECLRLQALNSR---LNCQAEWARRDSVGEVPPVPRVTVVSGIA 329
QY 204 -----DNVHLV-LNV---SEQHFGLSLYNQVQGPCKPRWHKNLTGPOITLNNHTDLP 254
DB 330 GEAKLDHLRLVSLGMRWCWDIEHYGLRIWF-----TDPDTGSILHLS--- 371
QY 255 CLCIQVWPLEPDSVRTNICPFREDPRAHQLWQAARLLTLTQSWLL-----DAPCS 306
DB 372 -----RSPRSEQENSPAATRELFSFOAGALAGGQIVSQAARKS 410
QY 307 LPAAALCWAPGDPGCPQLVP--PLSWENVTVDKVLEFPL-----LKGHPNLC 353
DB 411 ADGELLATR---NRLSSVPLSPDAPW-----RMLSAPLRQPGIVALREYLRQRPSC 460
QY 354 V-----QVNSSEKIQLOECL---WADSLGPKDDVLLLETRGPQDNRSICALEPSGCTSLP 406
DB 461 IRPLNQVDNLFILPVAECISLGDSSRQTL--DAQVISGEG-EDN--LLTL-----SLP 509
QY 407 SKASTRAA--RLGEYLLQDLSQGL-----QLWDDD----- 436
DB 510 ASASAPYAVERMAA--LLQQTDDPVCLVSGFVFDGQTLLEPQVMNTKTRAWALDAETAP 568
QY 437 ---LGALWACPMKDYIHKRWALVWLACLLFAAALLSILLKKD--HAKAARGRAALL 490
DB 569 VVASLPSASVLPVPSTAHO-----LLMRCQALLIOLLHNGRWYQBOGSAIGQAEALLA 619
QY 491 YSADDSGFERLVGALASALCOLPLRVAVDLWSRRELSSAQGPVAFHQAQRQTLOEGGVV 550
DB 620 NDLTAVGFYRLAHVL-----GQFNTESEARVEA 648
QY 551 LLFSPGVALCSEWL---ODGVSGPGAHGPHDAFRASLSCVLPD-----FLQGR 596
DB 649 M---NNGVLLCEQLFLLQOQGLNRPGF--PGECFICELR--LPDHRFRWKHNKLF--- 698
QY 597 APGSYVGACFDRLHDPDAVPALEFRTVPVFTLPQL 631
DB 699 -----EHGPAFPAL--VDCYTSPTPL 721

RESULT 10
Q9BYF6
ID Q9EYF6 PRELIMINARY; PRT; 745 AA.
AC Q9EYF6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 82.6 kDa protein.
GN YEHQ
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
```


RESULT 11		
Q9HZE5		
ID	Q9HZE5	PRELIMINARY; PRT; 1193 AA.
AC	Q9HZE5;	
DT	01-MAR-2001	(TrEMBLrel. 16, Created)
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)
DT	01-OCT-2001	(TrEMBLrel. 18, Last annotation update)
DE	Hypothetical protein PA3063.	
GN	PA3063.	
OS	Pseudomonas aeruginosa.	
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	
OC	Pseudomonas.	
OX	NCBI_TaxID=287;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-ATCC 15692 / PA01;	
RX	MEDLINE=2043737; PubMed=10984043;	
RA	Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,	
RA	Hickey M.J., Brinkman F.J., Hufnagle W.O., Kowalik D.J., Lagrou M.,	
RA	Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,	
RA	Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,	
RA	Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,	
RA	Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;	
RT	"Complete genome sequence of Pseudomonas aeruginosa PA01, an	
RT	opportunistic pathogen.";	
RL	Nature 406:959-964(2000).	
DR	EMBL; AE004730; AAG06451.1; -	
KW	Hypothetical protein; Complete proteome.	
SQ	SEQUENCE 1193 AA; 135097 MW; 1FE9553F34D3C191 CRC64;	
Query Match		
Best Local Similarity 3.1%; Score 114.5; DB 16; Length 1193;		
Matches 154; Conservative 53; Mismatches 240; Indels 263; Gaps 38;		
QY	81	DCLCRVAVHLVGHWE-----EPDEEKFGGAADSGV---EERNASLQAQV--- 126
DB	293	DLRLNWAAG-RVERAWEVGGELLALRPEDRTLADLARLGWGTONGPRALGFWKOLLAGA 351
QY	127	-----LSFQAYPTARCVLLEVQVPAALVQFGSVGVVYDCFEAALGSEVRIW- 174
DB	352	DDPALREHAWRLSLQMFDSATELLAPICAQOMTDEELDALVYSHETRGTPPEGEAWL 411
QY	175	-SYTPRYKE-----LNHTQOLPALP--WUNVSAGDNVHLVNLVNSEQHFGLS 221
DB	412	RGYVQ-RYPKORLAWORLQOILEHTQOQEBTGWARMAR-----HFPLSVKERMOWA-E 464
QY	222	LYWNQVGGPKPRWKNLNGPQIITLHNTDLVPCLCIQVWPLED-----SV 268
DB	465	THWNLFD--PRQW-KVLGAVDTAIREPEFWRLRAALAWALEQDDDAARAAYERMLADI 521
QY	269	RTN-----ICPFRED--PRAHONL---WQAAR-----LRLLTLSWLLDAPC--SILPA 309
DB	522	RLNSRDEQIALYRDSNPQALQVLIGSWQRSDPRRLASALQALNLDHWPALKSLLA 581
QY	310	EAALCWAPGGDPCPLVPPLSW-----ENVTVDKVLEFPPLKGHPNLC 353
DB	582	EAELPEAQGS-----PYWVARARLAEBQGHGDVAERLYREALVRF- 624
QY	354	VQVNSSEKLOQECW-----ADSLGP-----LKDDV-----LLETTRGP 388
DB	625	-----GENLVRELLWFYIDRGRRDSLAPLQWHLGALRDSTLWLPFASASLLE----- 675
QY	389	QDNRLC-----ALPSCGCTSLPSKASTRAARLGEYLLQDLOSG 427
DB	676	RNDQALAWERLYLKNPNDLVQAAADALDASG-----YQKALRLRLRLRL- 725
QY	428	QCLQLWDDDLGALWACPMDBKYIKRWALVWLACLLFAAALLSLIL-----LLKKDHAKAA 482
DB	726	-----DREAVRATPDS-----FATYRLRLVAVAQGPLLAQGEARRAW 761
QY	483	RGRAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELSAQGPVAMFHAQRROT 542
DB	762	NGEPAML-----QLWFEQFLDOLA-ATNQEPK--DNW-----LAWARGCLKI 802

RESULT 12		
Q96DW2		
ID	Q96DW2	PRELIMINARY; PRT; 657 AA.
AC	Q96DW2;	
DT	01-DEC-2001	(TrEMBLrel. 19, Created)
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)
DT	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)
DE	Similar to RecQ protein-like 4 (Fragment).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Lymph;	
RA	Strausberg R.;	
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC013277; AAH13277.1; -	
DR	InterPro; IPR001410; DEAD.	
DR	InterPro; IPR001650; Helicase_C.	
DR	Pfam; PF00271; Helicase_C; 1.	
KW	ATP-binding; Helicase.	
FT	NON_TER 1	
SQ	SEQUENCE 657 AA; 73415 MW; CF51B910F560CA18 CRC64;	
Query Match		
Best Local Similarity 3.0%; Score 112.5; DB 4; Length 657;		
Matches 115; Conservative 73; Mismatches 194; Indels 205; Gaps 31;		
QY	16	PVLSLERLVGPDATHCSPGLSC---RLWDSIL--CLPGDIVPAPGPVLAATHLQ--- 67
DB	68	PCYLRVCKVLRERMGVHCFLGLTATATRRRTASDVAQLAVAEEPDHLHGAPVPTNLHLSV 127
QY	68	-----TELVLRCQKETDCDCLRLRVAVHL--AVGHWEEDDEE 103
DB	128	SMRDTQALLTLLOKRFQNLDSIIICNRRDTE---RIALLRTCLHAAMVPGS--- 181
QY	104	KFGAADSQVEPRNASL-----QAQVLSFOAY-----PTARCVLLEV 142
DB	182	--GGRAPKTTAEAYHAGMCSRRRRVQRAFMOGQLRVVAVTAFVGMGLDRPDVRAV-LHL 238
QY	143	QVPAALVQFGSVGVVYDCFEAALGSEVRIWSYTPRYE--KELNHTQOLPALPWLNV 200
DB	239	GLPPSFESYVQAVGRAGRD-----GQPAHCHLFQPGQEDLRELRRHVHAUSDTEFLAVK 292
QY	201	ADGDNVHLVNV-----SEEQHFGLSLYWNQVQGP-PKPRW-----HKN 238
DB	293	-----RLVQVFPACTCTCTPPSEQE-----GAVGGERPVKYPQEAQLSHQA 338
QY	239	LTGPQIITLNTDLVPC-LCIQVWPLEPDSVRTNICPFREDPRAHONLQAARLRL--T 295
DB	339	APGPRVCMGHERALPIQLTVOALDMPDAIETLCYL-----ELPHHW-----LELLAT 390
QY	296	LQSWLLDAPCSLPAAALCWRAPE-----GGDPQC-----PLVPPPLSWENV 335
DB	391	YTHCLNCPGGAQLOALAHRCPPPLAVCLAQOLPEDPGOGSSSVVEFDVAVKLVDSHWELA 450
QY	336	TVDKVL-----EFPLLKGHPNLCVQVNSSEKLOQLOECLMADSLG 374
DB	451	SVRRALCOLQWDHEPRTGVRRGTGVLFVFESELAFLHRLSPGLTAEKQICDFLY---G 506
QY	375	PLKDDVLLLETRGPDQNRSLCALE-----PSGCTSLPSKASTRAAR---LGEY 419

Db 507 RVQ-----ARERQALRLRRTFOAFHSVAFFSGGCGLEQDDEERSTRLLKDLGRLY 556
QY 420 L-----LQDLOS-----GQC-LQLWDDDLGALWACPMKDYIHKR 452
Db 557 FEEEGQEPGGMEDAQGPFGQARLQDWEDQV-----RCDIRQFLSLR 599
RESULT 13
Q96F55 PRELIMINARY; PRT; 744 AA.
AC Q96F55;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Similar to RecQ protein-like 4 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Strausberg R.
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011602; AAH11602.1;
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR004589; RecQ.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR TIGRFAMs; TIGR00614; recq; 1.
KW ATP-binding; Helicase.
FT NON_TER 1
SQ SEQUENCE 744 AA; 82839 MW; 6AE0F90340A2C9F1 CRC64;

Query Match 3.0%; Score 112.5; DB 4; Length 744;
Best Local Similarity 19.6%; Pred. No. 1.1;
Matches 115; Conservative 73; Mismatches 194; Indels 205; Gaps 31;
QY 16 PVVLSLERLVQDATHCSFGLSC---RLWSDIL--CLPGDITVPAGPVLPATHLQ--- 67
Db 155 PCYLRVCKVLRRMGVHCFGLTATATRTASDAVQHLAAVEPDLHGAPVPNTLHLSV 214
QY 68 -----TELVRCQKETDCDLCRLRVAVHL--AVHGHWEPEDEE 103
Db 215 SMDRTDQALLTLLOGKRFQNLDSIIYCNREDTE---RIAALLRCLHAARVPGS--- 268
QY 104 KFGGAADSGVEEPRNASL-----QAQVLSFOAY-----PTARCVLLEV 142
Db 269 --GGRAPKTTAEAYHAGMCSRERRRRVQRAFMQGLRVVATVAFGMGLDRPDVRAV-LHL 325
QY 143 QVPAALYQFGQSVGVYDCFPAALGSEVRIWSYTPRYE--KELNHTQOLPALPWLNV 200
Db 326 GLPSSFESYQAVAGRGRD-----GQPAHCHLFLOPQGEDLRELRRHVHADSTDFLAVK 379
QY 201 AGDGNVHLVLNV-----SEEQHFGLSLYWNQVGP-PKPRW-----HKN 238
Db 380 -----RLVQRVFPACTCTTRPPEQE-----GAVGGERPVKYPQAEQLSHQA 425
QY 239 LTGPQIITLNLHTDLPVCLIQVWPLEPDSVRTNICPFREDPRAHNLQAAARLRL--T 295
Db 426 APGPRRCVCMGHERALPIQLTVQALDMPAEIETLCYL-----ELPHHW-----LELLAT 477
QY 296 LQSWLLDAPCSLPAEALCWAP-----GGDPQC-----PLVPPPLSWENV 335
Db 478 YTHCLRLNCPGPAQLQALAHRCPLAVLAQOLPEDPGGSSSVFDMVKLVDSMGWELA 537
QY 336 TVDKVL-----EFPLLKHPNLCVQVNSSEKLOLQCECLWADSLG 374
Db 538 SVRALCOLQWDHPRGVRGTGVLVFEFSELAPHLRSPGLDTAEKQICDFLY-----G 593
QY 375 PLKDDVLLLETRGPDNRSLCALE-----PSGCTSLPSKASTRAAR-----LGEY 419
Db -----

Db 594 RVQ-----ARERQALRLRRTFOAFHSVAFFSGGCGLEQDDEERSTRLLKDLGRLY 643
QY 420 L-----LQDLOS-----GQC-LQLWDDDLGALWACPMKDYIHKR 452
Db 644 FEEEGQEPGGMEDAQGPFGQARLQDWEDQV-----RCDIRQFLSLR 686
RESULT 14
Q87ZU1 PRELIMINARY; PRT; 405 AA.
AC Q87ZU1;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical protein PF1892.
GN PF1892.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010284; AAL82016.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 405 AA; 46019 MW; C68F3700FFLC615F CRC64;

Query Match 3.0%; Score 111.5; DB 17; Length 405;
Best Local Similarity 22.0%; Pred. No. 0.61;
Matches 87; Conservative 51; Mismatches 130; Indels 127; Gaps 21;
QY 325 PLVP-----PLSWENVTVDKVLEFP--LLKGHPNLCVQVNSSEKL--QLQECLEW 369
Db 64 PLVPPIQDGTQYMDSPLSWENVRIEDVIRFSLVLLGEAKVNVVVRKSKLIDSLQEL-- 121
QY 370 ADSLGLKDDVLLLETRGPQDNRSICALEPSCGTSILPSKASTRAARLGEVLLQDLQSGOC 429
Db 122 AMSIKPVDSEVLKE-----KPA-INILPEEFAPPLGRGKL-----KV 159
QY 430 LQLWDDDLGALWACP--MDKYIHKRWALVWLACLLFAAALSILLKKDHAKAAARGAA 487
Db 160 FKVVDNP-----KVPRKVDKTI-----SDELKA-----REA 185
QY 488 LL-LYSADDSGFER--LVGALASALCOLPLRVAVDLWS-----RRELSAQGPV 532
Db 186 IIGLY---ESGDEVYIIIRLSAGLLGVKKRIVPTPTWSITAVQDTIGNYLKRNILKNPII 242
QY 533 AWFHAQRRTQLQEGGVVLLFSPGAVALCSEWLOD---GVSPGGAHGHDAFRASLSVCL 589
Db 243 DNFEVYHHEFLGNRYVLLPWTYSFELLEWLKSLFGTSKPSVIHYEDPRG----- 296
QY 590 PDFLOGRA---PGSVVGACFDRL-----LHPDAVPALFRVPVFTLPSQLPD 633
Db 297 ---LKGAEQTTGAYAAARLSVLEVRKRKRQAGIIVREVTPTAYYAPGVQIRGVYKK 353
QY 634 FLGALQPPRAP-RSGRLQERAEQVSRLQPALDSY 667
Db 354 AL-----EKGPDKFENLAEALNQIGNILEHPLEEY 383

RESULT 15
Q9RY89 PRELIMINARY; PRT; 478 AA.
AC Q9RY89;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Hypothetical protein DR0061.
GN DR0061.
OS Deinococcus radiodurans.

Search completed: February 24, 2003, 09:24:47
Job time : 52 secs